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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

February 26, 2004, 08:18:56; Search time 10 Seconds (without alignments) 240.479 Million cell updates/sec

140 1 CGETYQSRVTHPHLPRALMRSTTKC 25 US-09-701-623C-5 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

283366 segs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Diri Diri Tras: * PIR 78:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		a			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ΙD	Description
-	117	00	428	н	вино	g eps
7	113	œ	426		I36948	D)
e	80	'n	429		EHRT	c
4	26	40.	107		m	gE chain C3 regi
ß	56	40	107		168726	3 regi
Q	26	40.	388		EHMS	Ig epsilon chain C
7	26	40.	548		S38864	in
00	54	m	684		360266	novel antigen rece
0	52	m	320		C86148	hypothetical prote
10	20	m	1597		865053	genome polyprotein
	20	m	1601		S48699	178K protein - tob
12	49.5	35.	1235		S16948	insulin receptor a
13	48	m	38		B31194	hypothetical prote
14	48	34.	1065		T52054	cellulose synthase
15	48	m	2254		D86215	protein T6D22.14 [
16	47.5	33.	381		S28115	gas-vesicle protei
17	47.5	33.	382		JQ1122	gas-vesicle protei
18	47.5	33	382		T08243	gas-vesicle operon
19	47	33.	242		MFIVCJ	matrix protein M1
20	47	33.	1940		804090	heavy
21	47	33.	1940		A24922	
22	47	33.	1940		A29320	myosin heavy chain
23	46.5	33.	1231		830185	insulin receptor s
24	46	32.	116		837909	cal
25	46	32.	247		A27547	trypsin (EC 3.4.21
26	46	32.	430		AG0531	cell cycle protein
27	46	•	550	Н	BEI	
28	46	32.	842	~	C83458	conserved hypothet
29	46	m	1019	N	361	conserved hypothet

MHC RTI.B-beta2 - hypothetical prote hypothetical prote MHC class II B-bet H-2 class II histo class II histocomp hypothetical prote hypothetical prote protein F25H2.6 [i myosin beta heavy myosin heavy chain myosin beta heavy myosin beta heavy myosin beta heavy myosin beta heavy myosin heavy chain	myosin heavy chain myosin heavy chain
154421 A03859 S76316 B76316 A60497 S10989 T222334 T21235 H87906 MWRBCB MRRCB A37102 S06006	138055 JX0178
44444444444444444444444444444444444444	24
93 106 210 245 264 264 264 343 1033 11934 11935 11935	1937
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0 11 0 18 18 18 18 18 18 18 18 18 18 18 18 18	. 4. 4. 6. 4. 7.

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Igropation chain C region - human (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: Homo sapiens (man) (Species: 31-Mar-1981 #sequence revision 13-Jun-1983 #text change 16-Jul-1999 (Spacession: A22771; A2315; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C40 R; Flanagan, J.G.; Rabbitts, T.H. EMBO J. 1, 655-660, 1982 T.H. EMBO J. 1, 655-660, 1982 T.H. Ajritle: The sequence of a human immunoglobulin epsilon heavy chain constant region general Ajreference number: A22771; MUID:84236029; PMID:6234164

A; Molecule type: DNA A; Residues: 1-428 cFLLA. A; Cross-references: GB: L00022; GB: U00227; GB: V00555; NID: 9185035 R; Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T. R; Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T. Britle: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudo; A; Reference number: A23195; MUID: 84207910; PMID: 6327276

A; Molecule type: DNA A; Residues: 2-428 <UED> A; Cross-references: GB: 40222; NID:g184755 B; Zhang, K.; Saxon, A.; Max, E.E. J; Exp. Med. 176, 233-243, 1992 A; Title: Two unmearal forms of human immunoglobulin E encoded by alternative RNA splicing A; Reference number: PH1214; MUID:92308839; PMID:1613458

A; Molecule type: DNA A; Residues: 320-428 <ZHA> A; Residues: 320-428 <ZHA> A; Cresidues: 320-428 <ZHA> A; Cresidues: 320-428 <ZHA> B; Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sug: Nucleic Acids Res. 11, 719-726, 1983 Nucleic Acids Res. 11, 719-726, 1983 A; Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon change and nucleotide sequencing of human immunoglobulin epsilon change and A; Reference number: A93491; MUID:83168897; PMID:6300763

A,Molecule type: mRNA A,Molecule type: mRNA A,Rosidues: 1-428 <SEN> A,Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035 Cell 29, 691-699, 1982 A,Title: Duplication and deletion in the human immunoglobulin epsilon genes. A,Reference number: A90824; MUID:83001945; PMID:6288268

A; Molecule type: DNA

A)Residues: 1-358,'L',360-428 <MAX>
A)Cross-references: GB:J00222; NID:g184755
A)Cross-reference difference may be due to polymorphism
A;Note: this sequence difference may be due to polymorphism
B;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
in Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-A;Reference number: A94418 A;Accession: A94418

A, Molecule type: protein

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Gaps

.. 0

Indels

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genes of chimpanzee and oranguta

; 0

Gaps

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Indels

Length 426;

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from rat immunoglobulin

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a epsilon chain C region - rat
fSpecies: Rattus norvegius (Norvay rat)
plate: 17-Dec-1982 #sequence revision 17-Dec-1982 #text_change 16-Jul-1999
fAccession: A93442; A90937; A02143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-0ct-1996 #sequence_revision 04-0ct-1996 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C)Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-200 (S)Accession: 136948 #S. Accession: 136948 #S. Accession:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 103/1; 209/1; 317/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;336-405/Domain: immunoglobulin homology <IMM>
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Nucleic Acids Res. 10, 6041-6049, 1982.
A;Title: Structure and evolution of the heavy chain fron
A;Reference number: A93442; MUID:83064537; PMID:6292865
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91.3%; Pred. No. 2.4e-09;
iive 1; Mismatches 1.
             0; Mismatches
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                                                                                                                                                                                                                              2 GETYQSRVTHPHLPRALMRSTTK 24
                                                                                                                                         2 GETYQSRVTHPHLPRALMRSTTK 24
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                          22; Conservative
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Riviellman, Riveracion of Grav inovel epsilon chain mRNA and a comparative analysis of A, Recession: C46536

A, Rocession: C46536

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A, Rederince is 282-394-426

A, Rederince is 282-394-426

A, Residues is 282-394

A, Residues in 294

A, Residues is 294

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A, Residues is 2
A; Residues: 'GAWTL',6,'X',8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',12 A; Experimental source: myeloma protein Nd S; Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; G Proc. Natl. Acad. Sci. U.S.A. '79, 6661-666, 1982
A; Title: Cloning and sequence determination of the gene for the human immunoglobulin eps A; Reference number: A99933; MUD:88065234; PMID:6815656
A; Accession: B93933
A; Molecule type: mRNA
A; Accession: B93933
A; Residence: 1-40; 68-114;427-428 < KEN>
A; Resid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: S02438
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 98-352 < IKE>
R;Zhang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
D Biol. Chem. 269, 456-462, 1994
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A;Reference number: A53116; MUID:94103254; PMID:8276835
A;Accession: A53116
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X;Residues: 320-428 <ZH2>
A;Esperimental source: myeloma U266-derived cell line AF-10
A;Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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A; Molecule type: mRNA
A; Residues: 'N',169-307,'L',309-342 <KIN>
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka;
hain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into l.
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;19-80/Domain: immunoglobulin homology <IM1>
F;118-186/Domain: immunoglobulin homology <IM2>
F;232-29/Domain: immunoglobulin homology <IM3>
F;327-398/Domain: immunoglobulin homology <IM3>
F;327-398/Domain: immunoglobulin homology <IM4>
F;46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                   A;Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, A;Reference number: A90937; MUID:83182019; PMID:6820340
A;Contents: myeloma IR162
A;Accession: A90937
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A;Molecule type: mRNA
A;Residues: 1-429 cHEL>
A;Reserimental source: strain LOU/c/Wsl, immunocytoma IR2
R;Kindsvogel, W R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
DNA 1, 335-343, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 57.1%; Score 80; DB 1; 1 Local Similarity 60.9%; Pred. No. 0.00025; les 14; Conservative 3; Mismatches 6
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Length 428;

Score 117; DB 1; Pred. No. 5.9e-10;

83.6%; 95.7%;

Query Match Best Local Similarity

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414 GYGYQCIVDHPDFPKPIVRSITK 436
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ses 11; Conservative
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C86148
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19g chain C3 region - mouse (fragment)

15g chain C3 region - mouse (fragment)

15g chain C3 region - mouse mouse)

15pcoies: Mus musculus (house mouse)

15pcoies: Mus musculus (house mouse)

15pcoies: Musculus (house immunoglobuli, H.; Honjo, T.; Okumura, K.

1mmunogenetics 27, 288-292, 1988

A; Timunogenetics 27, 288-292, 1988

A; Timunogenetics 154443; MuID:88152907; PMID:3346043

A; Accession: 168730

A; Accession: Is (B)

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1GB Chain C3 region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Accession: 168726

R;Shinhai, Y; Nakauchi, H; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-29, 1988

A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid a

A;Reference number: 154443; MuID:88152907; PMID:3346043

A;Status: preliminary; translated from GB/EMBU/DDBJ
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>
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A;Residues: 1.107 <RES>
A;Residues: 1.107 <RES>
A;Crose-references: GB:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>
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40.0%; Score 56; DB 2; Length 107;
Best Local Similarity 47.8%; Pred. No. 0.26;
Matches 11; Conservative 3; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYGYQCIVDHPDFPKPIVRSITK 105
|| || || || || || || GEGYQCRVDHPPFPRPIVRSITK 306
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A; Residues: 1-107 < RES>
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hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18 c'Superfamily: immunoglobulin C region; immunoglobulin homology (*Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin | F;1-44/Domain: immunoglobulin homology (fragment) < IML) < F;186-254/Domain: immunoglobulin homology < IMZ) < F;186-254/Domain: immunoglobulin homology < IMZ) < F;186-254/Domain: immunoglobulin homology < IMZ) < F;290-351/Domain: immunoglobulin homology < IMZ) < F;10,51,62,133,205,228,332,82/Binding site: carbohydrate (Asn) (covalent) #status pred
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Rigreenberg, A.S.; Avila, D.; Hughes, M.; Hughes, A.; McKinney, E.C.; Flajnik, M.P.
Rigreenberg, A.S.; Avila, D.; Hughes, M.; Hughes, A.; McKinney, E.C.; Flajnik, M.P.
A; Title: A new antigen receptor gene family that undergoes rearrangement and extensive A; Recesser antigen receptor gene family that undergoes rearrangement and extensive A; Recession: S60266; MUID: 95183140; PMID: 7877689
A; Accession: S60266
A; Status: preliminary; nucleic acid sequence not shown
A; Molecule type: mRMA
A; Molecule type: mRMA
A; Cross-references: EMBL: U18701; NID: 9699442; PIDN: AAB48195.1; PID: 9699443
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Accession: 33864
R;Kipp, B.; Becker, W.; Schlaak, M.
Schlaak, M
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C;Species: Ginglymostoma cirratum (nurse shark)
C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jul-2000
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47.8%; Pred. No. 0.98;
ive 3; Mismatches 9; Indels
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47.8%; Pred. No. 1.4;
cive 3; Mismatches
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FEBS Lett. 350, 5-8, 1994

A/Itle: Complete nucleotide sequence and genome organization of a tobamovirus infection A/Accession: S48699

A/Accession: 848699

A/Accession: 848699

A/Accession: 948699

A/Accession: 948699

A/Accession: 948699

A/Accession: 948699

A/Accession: 10101 < DORA

A/Accession: 1010 < DORA

A/Accession: 10101 < DORA

A/Accession: 1010 < DORA

A/Accession: 10101 < DORA

A/Ac
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NAlternate names: insulin receptor substrate pp185
C;Alternate names: insulin receptor substrate pp185
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
R;Sun, X.J; Rothenberg, P.; Kahn, C.R.; Backer, J.M.; Araki, E.; Wilden, P.A.; Cahill, Nature 352, 73-77, 1991
Nature 352, 73-77, 1991
A;Fitles: Structure of the insulin receptor substrate IRS-1 defines a unique signal tran A;Reference number: S16948; MUID:91287824; PMID:1648180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Accession: B31194
R;Zhan, X.; Bates, B.; Hu, X.; Goldfarb, M.
Roil. Biol. B; 3487-3495, 1988
A;Title: The human FGF-5 oncogene encodes a novel protein related to fibroblast growth
     R; Dorokhov, Y.L.; Ivanov, P.A.; Novikov, V.K.; Agranovsky, A.A.; Morozov, S.Y.; Efimov,
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A; Residues: 1-1235 < SGNN>
A; Residues: 1-1235 < SGNN>
A; Cross-references: EMBL:X58375; NID:g56503; PIDN:CAA41264.1; PID:g56504
A; Cross-references: EMBL:X58375; NID:g56503; PIDN:CAA41264.1; PID:g56504
B; Rothenberg, P.L.; Lane, W.S.; Karasik, A.; Backer, J.; White, M.; Kahn, C.R.
B; Biol. Chem. 266, 8302-8311, 1991
A; Title: Purification and partial sequence analysis of pp185, the major cellular
A; Reference number: A39811; MUID:91217066; PMID:2022647
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C'Species: Homo sapiens (man)
C'Date: 12-Jan-1989 #sequence_revision 12-Jan-1989 #text_change 05-Nov-1999
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Pred. No. 35;
4; Mismatches 6; Indels 1
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47.8%; Pred. No. 32;
live 1; Mismatches
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36.8%;
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Matches 11; Conservative
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Matches 14; Conserv
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NyAlternate names: RNA replicase
NyAlternate names: RNA replicase
NyAlternate names: RNA replicase
NyAlternate names: RNA replicase
Cypecies: Chinese rape mosaic virus
C;Species: Chinese rape mosaic virus
C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 17-Mar-1999
C;Accession: 1: Sanchez, F.; Martin Martin, A.; Martinez-Herrera, D.; Ponz, F.
R;Aquilar, I.; Sanchez, F.; Martin Martin, A.; Martinez-Herrera, D.; Ponz, F.
Plant Mol. Biol. 30, 191-197, 1996
A;Title: Nucleotide sequence of Chinese rape mosaic virus (ollseed rape mosaic virus), A;Teterence number: S65053; MUID:96197410; PMID:8616237
A;Accession: S65053
A;A
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Jun-2003
C; Accession: C86148.
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.P.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Atthors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Title: Sequence and analysis of chromosome lof the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: C86148
A; Retaus: preliminary
A; Molecule type: DNA
A; Residuse: Lype: DNA
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848699

178k protein - tobacco mosaic virus (strain cr-TMV)

178k protein - tobacco mosaic virus (strain cr-TMV)

N/Alternate names: readthrough protein

N/Contains: 122k protein

C;Species: tobacco mosaic virus, TMV

A;Variety: strain cr-TMV

C;Date: 06-Dec-1996 #sequence_revision 06-Dec-1996 #text_change 20-Sep-1999

C;Accession: S48699; 848659
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60.0%; Pred. No. 3.3;
tive 3; Mismatches
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C;Superfamily: acyl-CoA thioesterase II (TesB)
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Matches 9; Conserv
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Gaps

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Best Local Similarity 26.3%; Pred. No. 1e+02; Matches 5; Conservative 11; Mismatches
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C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Species: Arabidopsis thaliana (mouse-ear cress)
C'Accession: D86215
R'Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Huughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Liuros, J.S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, T.; Lin, X.; Liu, S.X.; Liu, Z.A.; Liuros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: D86215
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S:Function:
A;Description: BC 2.4.1.-; cellulose synthase [validated, MUID:98111412]; involved in as
C;Keywords: glycosyltransferase; hexosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Arioli, T.; Peng, L.; Betzner, A.S.; Burn, J.; Wittke, W.; Herth, W.; Camilleri, C.; Science 279, 717-720, 1998
A;Title: Molecular analysis of cellulose biosynthesis in Arabidopsis.
A;Reference number: Z13745; MUID:98111412; PMID:9445479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
T52054
Cellulose synthase (EC 2.4.1.-) catalytic subunit [validated] - Arabidopsis thaliana C,Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct.2000 #sequence_revision 20-Oct.2000 #text_change 31-Dec-2000
C;Accession: T52054
                                                                 A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-38 <ZHA>
A;Residues: 1-38 <ZHA>
A;Cross-references: GB:M23534; GB:M21617; NID:g806636; PIDN:AAB60698.1; PID:g182541
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A;Residues: 1-2254 <STO>
A;Cross-references: GB:AE005172; NID:g8778840; PIDN:AAF79839.1; GSPDB:GN00141
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Pred. No. 46;
1; Mismatches 9; Indels
                                                                                                                                                                                                                           Score 48; DB 2; Length 38;
Pred. No. 1.5;
0; Mismatches 4; Indels
A;Reference number: A31194; MUID:89096942; PMID:3211147 A;Accession: B31194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1055 <ABL>
A;Cross-references: EMBL:AF027174; PIDN:AAC39336.1
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Best Local Similarity 47.4%;
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Best Local Similarity 69.2%;
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 26, 2004, 08:17:40; Search time 6.4 Seconds (without alignments) 203.399 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-701-623C-5 140 1 CGETYQSRVTHPHLPRALMRSTTKC 25

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1 EPC HUMAN ID EPC HUMAN STANDARD; PRT; 428 AA. AC PO1854.		GN LGHE. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. RN 111 RN 111	RY MEDLINE-83168897; PubMed-6300763; RX MEDLINE-83168897; PubMed-6300763; RA Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K., RA Kikuchi M., Sugino Y., Nishida Y., Honjo T.; RT "Molecular cloning and nucleotide sequencing of human immunoglobulin RT epsilon chain cDNA."; R. Nucleic Acids Res. 11:719-726(1983).	3,2,2	RN 13.1 RY SEQUENCE FROM N.A. RX MEDLINE=84236029; PubMed=6234164; RA Flanagan J.G., Rabbitts T.H. RT "The sequence of a human immunoglobulin epsilon heavy chain constant RT region gene, and evidence for three non-allelic genes."; RI EMBO J. 1:655-660(1982).		RP PRELIMINARY SEQUENCE (MYELOWA PROTEIN ND). RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.; RL (In) Bach M.K. (eds.); RL Immediate hypersensitivity: modern concepts and developments, pp.1-36, R. Marcel Dekker, New York (1978).	RN 16) RX MEDLINE-83065234; PubMed=6815656; RX MEDLINE-83065234; PubMed=6815656; RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J., RA Bell L.O., Gould H.J.; RT "Cloning and sequence determination of the gene for the human RT immunoglobulin epsilon chain expressed in a myeloma cell line."; RI Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
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                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its concent is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                       PRR, AZZ771; EMHU.
PRB, 11GE; 15-UTL-92.
PRB, 11GE; 15-UTL-92.
RPB, 10GV; 18-SED-01.
RG-10GV; 18-SED-10GHE.
RG-10GV; 19-SED-10GHE.
RG-10GV; 10G-10GHE.
RG-10GFE.
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M -> L (POSSIBLE POLYMORPHISM).
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              MEDLINE=67089848; PubMed=3796618;
Padlan E.A., Davies D.R.;
"A model of the Fc of immunoglobulin E.";
MOI. Immunol. 23:1063-1075(1986).
MOI. SIMILARITY: Contains 4 immunoglobulin-like domains.
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
21-JUL-1986 (Rel. 01, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g epsilon chain C region.
Rattus norvegicus (Rat).
Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
11)
11]
12AID=10116;
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MBDLINE=83046137; bubMed=6292865;
MBDLINE=83046137; bubMed=6292865;
Hellman L., Pettersson U., Engstroem A., Karisson T., Bennich H.,
"Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
MEDLINE=83182019; PubMed=6820340;
Kindavogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.,
"A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:
construction, identification, and DNA sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 117; DB 1; Length 42
Pred. No. 2.2e-10;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47019 MW; 25C4CA072AA558A0 CRC64;
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Best Local Similarity 95.7%;
Matches 22; Conservative
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418
428 AA;
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us-09-701-623c-5.rsp

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421 AA;
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hes 11; Conserv
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198
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MEDLINE=84236092; PubMed=6329728;
Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
"The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with the Numan epsilon gene sequence.";
EMBO J. 1:1117-1123(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POG336, PO1856;
21-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 33, Last sequence update)
15-UTL-1996 (Rel. 33, Last sequence update)
15-UTL-1999 (Rel. 38, Last annotation update)
16 epsilon chain C region.
18 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mush. 13xID=10090;
Hellman L., Pettersson U., Bennich H.; "Characterization and molecular cloning of the mENA for the heavy "Characterization and molecular cloning of the menoglobulin E."; Proc. Natl. Acad. Sci. U.S. A. 79:1264-1268(1982).
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MEDLINE-83117774; PubMed-6818553;
Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
"Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.";
Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
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0
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HSSP, P01854; LIGE.
InterPro; IPR00110; Ig-like.
InterPro; IPR003006; Ig_c1.
InterPro; IPR003006; Ig_MHC.
Pfam; PP00047; ig; 4.
SMART; SM00407; ig; 4.
SMOSTIE; PS00290; IG_MHC; 3.
Immunoglobulin domain; Immunoglobulin C region; Repeat.
NON TER

6 89 IG-LIKE 1.
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Pred. No. 0.0001;
3; Mismatches 6; Indels
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IG-LIKE 2.

IG-LIKE 4.

IG-LIKE 4.

R -> N (IN REF. 2).

P -> L (IN REF. 2).

W, D2970B34EF8A72B0 CRC64;
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Best Local Similarity 60.9%;
Matches 14; Conservative
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205
314
168
308
429 AA;
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SEQUENCE
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16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
18-EBB-2003 (Rel. 40, Last annotation update)
RNA-directed RNA ploinmerse (EC 2.7.7.48) (182 kDa protein) [Contains: Methyltransferase/RNA helicase (MT/HEL) (125 kDa protein)].
Chinese rape mosaic virus (CRNV) (Oilseed rape mosaic virus).
Viruses, seRNA positive-strand viruses, no DNA stage; Tobamovirus.
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MEDLINE-96197410; PubMed=8616237;
Aguilar I., Sanchez F., Martin-Martin A., Martinez-Herrera D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEGMI, PF00047; ig; 4.
SMART; SM00407; ig; 4.
PROSITE; PS00290; IG_MRC; 3.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
NON TER
DOMAIN 1 90 CH1.
DOMAIN 198 304 CH3.
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llarity 47.8%; Pred. No. 0.47;
Conservative 3; Mismatches 9; Indels
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CH2.
CH3.
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PIR; A02145; EHMS.
HASP, P01854; IJGE.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003066; Ig_MHC.
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                                                        Sacks D.B.
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MOD_RES
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Matches
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FUNCTION: THE SMALLER PROTEIN IS A METHYLTRANSFERASE ACTIVE IN RNA CAPPING AND AN RNA HELICASE.
CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
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MEDITNE=94067102; PubMed=7504175;
MEDITNE=94067102; PubMed=7504175;
Sun X.J., Crimmins D.L., Myers M.G., Miralpeix M., White M.F.;
"Pleiotropic insulin signals are engaged by multisite phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Wilden P.A., Cahill D.A., Goldstein B.J., White M.F.;
"Structure of the insulin receptor substrate IRS-1 defines a unique
                                                                                                (RNA)(N)
MISCELLANBOUS: READTHROUGH OF THE TERMINATOR CODON UAG OCCURS
BETWEEN CODONS FOR GLN-1103 AND GLN-1105.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase, RNA-directed RNA polymerase, Helicase, ATP-binding.
CHAIN 1 1597 RNA-DIRECTED RNA POLYMERASE.
CHAIN 1103 METHYLTRANSFERASE/RNA HELICASE.
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Pred. No. 16;
4; Mismatches 6; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1597 AA; 181621 MW; 7256A908BD3308F2 CRC64;
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Ol-UUN-1994 (Rel. 29, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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V -> G.
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STRAIN-Sprague-Dawley; TISSUE-Liver;
MEDLINE-91287824; PubMed-1648180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR, S65053; S65053. RNA dep RNApol2. InterPro; IPR001789; RNA_pol_DS_PS. InterPro; IPR007099; RNA_pol_DS_PS. InterPro; IPR007099; RNA_pol_PS_vir. InterPro; IPR005069; V methyItransf. InterPro; IPR000606; Viral_helicasel. Pfam; PF00978; RNA_dep_RNApol2; 1. Pfam; PF01443; Viral_helicasel; 1. Pfam; PF01660; VmethyItransf; 1.
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IRS1 OR IRS-1.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U30944; AAB60599.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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919
1286
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PHOSPHORYLATION SITES.
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919
1286
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VARIANT
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IRS1 RAT
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                                                                                                                                                                                  domains
MEDLINE-93352637; PubMed-8349691;
Tanasijevic M.J., Myers M.G., Thoma R.S., Crimmins D.L., White M.F.,
                                                                                                                                       processes
                                                                     "Phosphorylation of the insulin receptor substrate IRS-1 by casein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                          kinase II.";
J. Biol. Chem. 268:18157-18166(1993).

-:- FUNCTION: May mediate the control of various cellular proce-
insulan. When phosphorylated by the insulan receptor binds
insulan. When phosphorylated by the insulan receptor binds
specifically to various cellular proteins containing SH2 do
specifically to various cellular proteins containing SH2 do
such as phosphatidylinositol 3-kinase p85 subunit or GRB2.
-:- SIMILARITY: Contains 1 PH domain.
-:- SIMILARITY: Contains 1 PTB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
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PHOSPHORYLATION
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47.8%; Pred. No. 15;
tive 1; Mismatches
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PTB.
POLY-GLN.
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PIR, S16948; S16948.
HSSP, P35684, ILRS.
INTERPRO, IPR002404; Insin_receptorS1.
INTERPRO; IPR001494; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             816 CGARPESSVTHPHHALQPHLPR 838
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Pfam; PF00169; PH; 1.
PRINTS; PR00628; INSULINESI.
SMART; SM00233; PH; 1.
PR0SITE; PS50003; PH DOMAIN; 1.
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SEQUENCE FROM N.A.
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STRAIN-RRC-1: PLASHUD-DNRC100;
STRAIN-RRC-1: PLASHUD-DNRC100;
NG W.V.; Ciufo S.A., Smith T.M., Bumgaxner R.E., Baskin D., Faust J.,
Hall B., Loretz C., Sero J., Slagel J., Hood L., DasSarma S.;
"Snapshot of a large dynamic replicon in a halophilic archaeon:
megaplasmid or minichromosome?";
Genome Res. 8:1131-1141(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GWCI HALNI STANDARD; PRT; 382 AA.
P24574 (OSHIT);
01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
03-PEB-2003 (Rel. 41, Last annotation update)
GGS vesicle protein C 1.
Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and Plasmid pNRC100, Plasmid pNRC100, Plasmid pNRC100, Plasmid pNRC200, and Plasmid pHH1.
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaces; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=NRC-1; PLASMID=PNRC100;
MEDLINE=91323716, PubMed=1864501;
Jones J.G., Young D.C., Dassarma S.;
Structure and organization of the gas vesicle gene cluster on Halobacterium halobium plasmid pNRC100.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ή,
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Sbrogna J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 47.5; DB 1; Length 381;
Pred. No. 8.4;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                              APPROXIMATE TANDEM REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                       ASP/GLU-RICH (ACIDIC).
9FB48199D0305921 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berguist B.,
Thorsson V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20504483; PubMed=11016950;
Ng W.V., Kennedy S.P., Mahairas G.G.,
Shukla H.D., Lasky S.R., Baliga N.S.,
                                                                                                                                                                        EMBL; X64701; CAA45944.1; -. PIR; S28115; S28115; S28115. InterPro; IPR008639; Halo GVPC. Pfam; PF05465; Halo_GVPC; 1.
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STRAIN=NRC-1; PLASMID=pNRC200;
                                                                                                                                                                                                                                                                                                                                                                                                                          42653 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 64.3
9; Conservative
                                                                                                                                                                                                                                                 Gas vesicle; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                          381 AA;
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CYANOBACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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Best Local
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                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are the EMBL outstations on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license apreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=DSM 1411;
MEDLINE=93021102; PubMed=1404376;
Englert C., Krueger K., Offiner S., Pfeifer F.;
"Three different but related gene clusters encoding gas vesicles in
              Jong M.T.C., Carey A.H., Caldwell K.A., Lau M.H., Handel M.A., Driscoll D.J., Stewart C.L., Rinchik E.M., Nicholls R.D., "Imprinting of a RING zuc-finger encoding gene in the mouse chromosome region homologous to the Prader-Willi syndrome genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COF
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SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 34.3%; Score 48; DB 1; Length 544; Local Similarity 45.0%; Pred. No. 10; es 9; Conservative 4; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Halobacterium mediterranei (Haloferax mediterranei).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Haloferax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3H1-TYPE 3.
FF05B7D034C5EA9F CRC64;
                                                                                                            Hum. Mol. Genet. 8:795-803(1999).
-i- SINLIARITY: Contains 1 RING-type zinc finger.
-i- SIMILARITY: Contains 3 C3H1-type zinc fingers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C3H1-TYPE 1.
C3H1-TYPE 2.
MAKORIN-TYPE CYS-HIS.
RING-TYPE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-BFB-2003 (Rel. 41, Last annotation update)
Gas vesicle protein C.
MEDLINE=99214019; PubMed=10196368;
                                                                                                                                                                                                                                                                                                EMBL, U19106; AAA76863.1; -...
EMBL, U19106; AAA76863.1; -...
InterPro; IPR001841; Znf_CCCH.
InterPro; IPR011841; Znf_CCCH.
Ffam; PF00097; Zf_C3HC4; 1...
Fram; PF00042; Zf_CCCH; 3...
SMART; SM00184; RING; 1...
PROSITE; PS00518; ZF_CSH1; 3...
PROSITE; PS00518; ZF_RING 1; 1...
PROSITE; PS00518; ZF_RING 1; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  226 GOPYRGRVVPPHGPEAPLQS 245
                                                                                        region.";
Hum. Mol. Genet. 8:795-803(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59444 MW;
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ZN_FING
SEQUENCE
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ZN_FING
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Gaps

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Weiss A., Schiaffino S., Leinwand L.A.;
"Comparative sequence analysis of the complete human sarcomeric myosin heavy chain family: implications for functional diversity.";
J. Mol. Biol. 290:61-75(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Extraocular muscle;
MEDLINE=99026150, PubMed=9806854;
Winters L.M., Briggs M.M., Schachat F.;
Winters L.M., Briggs M.M., Schachat F.;
The human extraocular muscle myosin heavy chain gene (MYH13) maps to the cluster of fast and developmental myosin genes on chromosome 17.";
Genomics 54:186-186 (1998).
-!- FUNCTION: Muscle contraction.
-!- SUBUNIT: Muscle myosin is a hexameric protein that consists of 2
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=88300888; PubMed=3404579;
Yamashita M., Krystal M., Palese P.;
"Evidence that the matrix protein of influenza C virus is coded for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ouco sagratus naudumin.
Eukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9UKÄ3; O95252;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myosin heavy chain, skeletal muscle, extraocular (MyHC-eo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 1; Length 242;
Pred. No. 6.1;
4; Mismatches 7; Indels
                                                                                                                                  Influenza C virus (strain C/JJ/50).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenzavirus C.
NCGE_TAXID=11560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 AA; 26967 MW; ABF9D9054E1C9D91 CRC64;
                          01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1938 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNHTFGSNIMRPHLEKAI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1917-1938 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGETYQSRVTHPHLPRAL 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M22038; AAA43781.1; -.
PIR; A28878; MFIVCJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.6%;
                                                                                                                                                                                                                                                                                                                                         by a spliced mRNA.";
J. Virol. 62:3348-3355(1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 38.>*,
Best Local Similarity 38.>*,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Extraocular muscle;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fik; AZ88/8; Mrivoj.
InterPro; IPR004271; CM1.
Pfam; PF03026; CM1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matrix protein.
SEQUENCE 242
                                                                                              Matrix protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; A28878;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209
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MYHD_HU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Mol. Biol. 227:586-592(1992).

-!- FUNCTION: May confer stability to the gas vesicle membranes, Gas vesicles are small, hollow, gas filled protein structures that are found in several microbial planktonic microorganisms. They allow the positioning of the organism at the favorable depth for growth.
-!- SUBCELLULAR LOCATION: Binds to the external surface of the gas
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.B., Krebs W.P., Angevine C.M., Dale H., Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Unng K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1."; Paroc. Natl. Acad. Sci. U.S.A. 97:12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=NRC-817; PLASMID=PHH1;
MEDLINE=93021102; PubMed=1404376;
Englert C., Krueger K., Offiner S., Pfeifer F.;
"Three different but related gene clusters encoding gas vesicles in
                                                                                                                                                                                                                          STRAIN=NRC-817; PLASMID=pHH1;
MEDLINE=92065812; PubMed=1956294;
HOTNE M., Englert C., Winmer C., Pfeifer F.;
HATNE M. Englen G. 9 kbp contains all genes necessary for gas vesicle synthesis in halophilic archaebacteria.";
MOI. Microbiol. 5:1159-1174(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vesicle membrane.
SMILLARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF
CYANOBACTERIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; T08243; T08243.
InterPro; IPR008639; Halo GVPC.
Pfam; PF05465; Halo GVPC, 1.
Gas vesicle; Plasmid; Repeat; Complete proteome.
284 7 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 47.5; DB 1; Length 382; Pred. No. 8.4; 2; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ASP/GLU-RICH (ACIDIC).
171DBEB4C0364F46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M58557; AAA98197.1; -.
EMBL; AF016485; AAC82810.1; -.
EMBL; AE005142; AAG2077.1; -.
EMBL; X57161; CAA40451.1; -.
EMBL; X64729; CAA45981.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42391 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGEYYQA-ITEPHL 356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 halophilic archaea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131
169
201
241
254
382 AA;
                                                                                                                                                                                                         SECUENCE FROM N.A.
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VMAT_INCJJ
VMAT_INCJJ
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SEQUENCE
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REPEAT REPEAT

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Gaps

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NCBI_TaxID=9031;
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VARIANT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
DOMAIN
NP_BIND
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BR HUSE; PAIS38; 2MYS.

BR Genew; HGNC:7571; MYH13.

R Gord, GO1005854; F.actin binding; NAS.

GO; GO:0005524; F.ATP binding; NAS.

GO; GO:0005524; F.ATP binding; NAS.

GO; GO:0005524; F.ATP binding; NAS.

GO; GO:0005516; F.calmodulin binding; NAS.

BROGOSTI IRRO02928; Myosin_tail.

BR Ffam; PPO0612; IQ; 1.

BR Ffam; PPO0615; Myosin_bad; 1.

BR Ffam; PPO1576; Myosin_had; 1.

BR Ffam; PRO155; Myosin_had; 1.

BR Ffam; PRO155; Myosin_had; 1.

BR RINTS; PRO10193; MYOSINHEAD.

BR SNART; SM000142; MYSC; 1.

BROSITE; PSS0096; IQ; 1.

RW PROSITE; PSS0096; IQ; 1.

RW PROSITE; PSS0096; IQ; 1.

RW PROMIN; ARP-binding; ATP-binding; McHylation; Multigene family.

BR DOMAIN 785 B14 IQ; 1.

BOMAIN 785 B14 IQ; 1.
heavy chain subunits (MHC), 2 alkali light chain subunits (MLC) and 2 regulatory light chain subunits (MLC-2).

SUBCELLULAR LOCATION: Thick filaments of the myofibrils.

DOMAIN: The rodilke tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides, characteristic for alpha-helical coiled coils.

MISCELLANEOUS: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped subfragment (S2).

SIMILARITY: Contains 1 myosin-like globular head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATP (POTENTIAL).
ACTIN-BINDING (BY SIMILARITY).
ACTIN-BINDING (BY SIMILARITY).
METHYLATION (TRI-). (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.6%; Score 47; DB 1; Length 1938; 52.9%; Pred. No. 58; ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223678 MW; 1F6D006416381CD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IQ.
COILED COIL (POTENTIAL).
                                                                                                                                                                RESULT 11

MYATA CHICK STANDARD; PRT; 1940 AA.

AC PO2565;

DT 21-UUL-1986 (Rel. 01, Created)

DT 01-FBE-1996 (Rel. 31, Last sequence update)

DT 15-MAR-2094 (Rel. 43, Last annotation update)

DT 15-MAR-2094 (Rel. 43, Last annotation update)

DF Myosin heavy chain, fast skeletal muscle, embryonic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      667 RSTHPHFVRCLIPNETK 683
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RVTHPHLPRALMRSTTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 52.>
Best Local 9; Conservative
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843 1931
179 18
659 68
761 77
130 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOD RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
NP BIND
DOMAIN
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Signature gallue (Thicken)

Shakayora Meazaca, Chordata, Cranata, Vertebrate, Buteleostomi, Charlesuria, Aves, Neograthee, Galliformes, Phasianidae, Phasianinae, Mallue, Mallue, Mallue, Chordata, Callick, Mallue, M
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1331 133
1331 133
1508 160
1663 166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYH3 RAT
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NP BIND
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                            Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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MISCELLANEOUS: Bach myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped
                                                                                                                                                                                                                                                                                                                                      MYH3 HUMAN STANDARD; PRT; 1940 AA.
P11055; Q15492;
01-UTL-1989 [Rel. 11, Created)
01-UTL-1989 (Rel. 43, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
Myosin heavy chain, fast skeletal muscle, embryonic (Muscle embryonic myosin heavy chain) (SMHCE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDINE-8956648; PubMed=2771643;
MEDINE-89366648; PubMed=2771643;
MEXATECHINE-89366648; PubMed=2771643;
MEXATECHINE-89366648; DubMed=2771643;
"Expression and DNA sequence analysis of a human embryonic skeletal muscle myosin heavy chain gene.",

"Le FUNCTION: Muscle contraction.

-: SUBUNIT: Muscle myosin is a hexameric protein that consists of 2 heavy chain subunits (MEC).

-: SUBUNIT: Muscle myosin is a hexameric protein that consists of 2 heavy chain subunits (MEC).

-: SUBUNIT: Abundant (MHC), 2 alkali light chain subunits (MLC).

-: SUBCELLUAR LOCATION: Thick filaments of the myofibrils.

-: SUBCELLUAR LOCATION: Thick filaments of the myofibrils.

-: SUBCELLUAR LOCATION: Thick filaments of the myofibrils.

-: DEVELOPMENTAL STAGES: Abundantly present in fetal skeletal and not present or barely detectable in heart and adult skeletal
                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nomo deptens vienna.).
Bukaryota, Metazomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90033298; PubMed=2806546;
Eller M.S., Stedman H.H., Sylvester J.E., Fertels S.H., Wu Q.-L.,
Eller M.S., Stedman H.H., Sylvester J.E., Fertels S.H., Wu Q.-L.,
Eaychowdhury M.K., Rubinstein N.A., Kelly A.M., Sarkar S.,
"Human embryonic myosin heain cDNA. Interspecies sequence
conservation of the myosin rod, chromosomal locus and isoform
specific transcription of the gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDILIBE-89263803; PubMed=2726495;
Eller M.S., Stedman H.H., Sylvester J.E., Fertels S.H.,
Rubinstein N.A., Kelly A.M., Sarkar S.;
"Nucleotide sequence of full length human embryonic myosin heavy
chain CDNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arnold H.H.; "Identification of three developmentally controlled isoforms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Skeletal muscle;
MEDLINE=90235862; PubMed=1691980;
Bober E., Buchberger-Seidl A., Braun T., Singh S., Goedde H.W.,
                                                                                                                     ;
                                                                 Score 47; DB 1; Length 1940;
Pred. No. 58;
2; Mismatches 6; Indels
ERA -> GRT (IN REF. 2).
W; C34833D75B04DFF2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 17:3591-3592(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myosin heavy chains.";
Eur. J. Biochem. 189:55-65(1990);
1915 ERA
1, 222816 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 856-1940 FROM N.A.
                                                                                                                                                                                                 668 RSTHPHFVRCLIPNETK 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 774-1940 FROM N.A.
                                                                                                                                                                       8 RVTHPHLPRALMRSTTK 24
                                                                   33.6%;
Similarity 52.9%;
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'BBS Lett. 256:21-28(1989).
1913 191
1940 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chain cDNA
CONFLICT
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                                                                                                                          Matches
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Myosin; Muscle protein; Coiled coil; Thick filament; Actin-binding; Calmodulin-binding; ATP-binding; Methylation; Multigene family. DOMAIN 1781
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COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTENTIAL).
subfragment (S2).
-!- SIMILARITY: Contains 1 myosin-like globular head domain.
-!- SIMILARITY: Contains 1 IQ domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.6%; Score 47; DB 1; Length 1940; 47.1%; Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 A -> G (IN REF. 3).

92 KK -> QE (IN REF. 1 AND 2).

93 SR -> RA (IN REF. 3).

94 RG -> QT (IN REF. 2).

224035 MW; 43CASGC6A4BA1253 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
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01-0CT-1989 (Rel. 12, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Myyosin heavy chain, fast skeletal muscle, embryonic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1940 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM. 16720. P. Muscle development; TAS GO; GO:0007517, P. muscle development; TAS GO; GO:0007517, P. muscle development; TAS InterPro; IPR001609; Myosin_N. InterPro; IPR004609; Myosin_N. InterPro; IPR004609; Myosin_N. InterPro; IPR002928; Myosin_N. InterPro; IPR002928; Myosin_Lail. Pfam; PF00213; Myosin_head; 1. Pfam; PF00176; Myosin_Lail. InterPro; PF00136; Myosin_Lail. ProDom; PF001536; Myosin_Lail. InterProDom; PF001536; Myosin_Lail. InterProDom; PF001536; Myosin_head; 1. SMART; SM001515; IQ; 1. SMART; SM00242; MYSC; 1. PROSITE; PS50096; IQ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    664 RTTHPHFVRCIIPNETK 680
                                                                                                                                                                                                                                                                                             EMBL; X13988; CAA32167.1; -.
EMBL; X13100; CAA31492.1; -.
EMBL; X51593; CAA35942.1; -.
EMBL; X15696; CAA37311.1; -.
PIK; S04099; S04090.
HSSP; P13538; 2MYS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 RVTHPHLPRALMRSTTK 24
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8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                               P13538; 2MYS.
HGNC:7573; MYH3.
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SEQUENCE FROM N.A.
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.0-OCT-2003 (Rel. 42, Last annotation update)
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0
                                                  Nadal-Gunard B.;

Nadal-Gunard B.;

Nadal-Gunard B.;

"Complete nuclectide and encoded amino acid sequence of a mammalian myosin heavy chain gene. Evidence against intron-dependent evolution of the rod.";

J. Mol. Biol. 199:291-317(1986).

-!- FUNCTION: Muscle contraction.

-!- FUNCTION: Muscle contraction.

-!- FUNCTION: Muscle contraction.

-!- FUNCTION: Muscle myosin is a hexameric protein that consists of 2 and 2 regulatory light chain subunits (MLC-2).

-!- SUBJUNIT: Muscle myosin is a hexameric protein that consists of 2 and 2 regulatory light chain subunits (MLC-2).

-!- SUBJUNIT: Muscle myorin subunits of the myofibrils.

-!- DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides.

-!- DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptides.

-!- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light meromyosin (LMM) and 1 heavy meromyosin (HMM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped subfragment (S2).

-!- SIMILARITY: Contains 1 myosin-like globular head domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R HISSP, P1358, 2MYS.

R HISSP, P1358, 2MYS.

R InterPro; IPR000048; IQ_region.

R InterPro; IPR0001609; Myosin_head.

R InterPro; IPR002928; Myosin_tail.

R InterPro; IPR00212; IQ; Spectrin.

R Ffam; PF00612; IQ; Spectrin.

R Ffam; PF00133; Myosin_tail.

R Pfam; PF00135; Myosin_tail.

R PRINTS; PR00193; MYOSINHEAVY.

R ProDom; PF001955; Myosin_tail.

R PROSTITS; PR00195; IQ; 1.

R MART; SM00105; IQ; 1.

R MART; SM00105; IQ; 1.

R MART; SM00142; MYSC; 1.

R PROSTITE; PS50096; IQ; 1.

R Myosin; Muscle protein; Colled coil; Thick filament; Actin-binding; Mcthylation; Multigene family.

T DOMAIN.

T DOMAIN.
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                    Strehler B.E., Strehler-Page M.-A., Perriard J.C., Periasamy M.,
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Pred. No. 58;
3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223857 MW; B5D546A596E5A696 CRC64;
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COLLED COLL (POTENTIAL).
ATP (POTENTIAL).
ACTIN-BINDING.
ACTIN-BINDING.
ACTIN-BINDING.
METHYLATION (TRI-) (POTEN'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 29, Created)
(Rel. 29, Last sequence update)
MEDLINE=87060988; PubMed=3783701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | |||| | :::||
664 RTTHPHFVRCIIPNETK 680
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PIR; A24922; A24922.
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Best Local Similarity 4/...
Best Local 8; Conservative
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656
656
77
130
130 AA;
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P35569;
01-JUN-1994 (
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cloning.";
Biophys. Acta 1172:323-326(1993).
Biochim. Biophys. Acta 1172:323-326(1993).
-!- FUNICION: May mediate the control of various cellular processes binsulin. When phosphorylated by the insulin receptor binds specifically to various cellular proteins containing SH2 domains such as phosphatidylinositol 3-kinase p85 subunit or GRB2.
-!- SIMILARITY: Contains 1 PH domain.
                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=94220494; PubMed=8167159;
ATAXI E., Haag B.L. III, Kahn C.R.;
"Cloning of the mouse insulin receptor substrate-1 (IRS-1) gene and complete sequence of mouse IRS-1.";
Biochim. Biophys. Acta 1221:353-356(1994).
                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=93192326; PubMed=8448209;
Keller S.R., Aebersold R., Garner C.W., Lienhard G.E.;
"The insulin-elicited 160 Map phosphotyrosine protein in mouse
adipocytes is an insulin receptor substrate 1: identification by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLY-SER.
POLY-GLN.
POLY-GLN.
POLY-GLN.
POLY-BO.
PHOSPHORYLATION (BY CK2)
(BY SIMILARITY).
PHOSPHORYLATION (BY INSR)
(BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X69722; CAA49378.1; -. PIR; S30185; S30185. PDB; 1AYE; 31-AUG-94. MCD; MG1:99454; Irsl. InterPro; IPR002404; Insln_receptorS1. InterPro; IPR001849; PH. Fam; PF02174; IRS; 1. Pfam; PF02174; IRS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS, PRO0628; INSULINRSI.
SMART; SM00233; PH; 1.
SMART; SM00310; PTB; 1.
PROSTITE, PSS50003; PH DOMAIN; 1.
Phosphorylation; 3D-Etricture.
Insulin receptor substrate-1.
IRS1 OR IRS-1.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L24563; AAA39335.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                              NCBI_TaxID=10090;
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us-09-701-623c-5.rsp

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                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                            Query Match 33.2%; Score 46.5; DB 1; Length 1233; Best Local Similarity 43.5%; Pred. No. 42; Matches 10; Conservative 2; Mismatches 4; Indels 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-UTW-1994 (Rel. 29, Created)
01-UTW-1994 (Rel. 29, Last sequence update)
01-UTW-1994 (Rel. 29, Last amnotation update)
01-UTW-1994 (Rel. 29, Last amnotation update)
Hypothetical 13.6 kDa protein in MDHI-VMAS intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
32.9%; Score 46; DB 1; Length 116;
Best Local Similarity 45.0%; Pred. No. 3.9;
Matches 9; Conservative 3; Mismatches 8; Indels
1220 1220 PHOSPHORYLATION (BY INSR)
1038 1039 MISSING (IN REF. 2).
1182 1182 H -> R (IN REF. 2).
1233 AA; 130723 MW; COE952D890DADD87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
Pohl T.M., Pohl F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGINOLINI, IZ. 12004W.
SGINOLINI, IZ. 12004W.
INTERPRO, IPRO08913; ZF-CHY.
Pfam, PF05495; Zf-CHY; 1.
Hypothetical protein.
SEQUENCE 116 AA; 13641 MW; 57464E5FD9A591F8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            || :| :||
816 CGARPESSLTHPHHHVLQPHLPR 838
                                                                                                                                                                                                                                                                                                                                                                                           1 CGETYQSRVTH-----PHLPR 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
YK14 YEAST
TO 11-JUN-1994
DT 01-JUN-1994
DT 01-JUN-1994
DT 01-JUN-1994
DT 01-JUN-1994
DT 01-JUN-1994
DE HYPOTHERICAL
OS SACCHAROMYCE
OC SACCHAROMYCE
OC NCBI_TAXID=4
RN [1]
CC NCBI_TAXID=4
CC HAELYOPEN
CC This SWISS-F
C
                                                                             CONFLICT
CONFLICT
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Search completed: February 26, 2004, 08:24:18 Job time : 8.4 secs

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Q91tk6 arabidopsis Q99tk6 arabidopsis Q9485 drosophila Q918n3 rana pipien Q918n3 rana pipien Q918n3 rana pipien Q918d arabidopsis Q96tk6 arabidopsis Q809a2 crucifer to Q809a2 crucifer to Q804b2 crucifer to Q81k0 arabidopsis Q91k0 arabidopsis Q91k0 arabidopsis Q91k5 influenzavi Q9465 influenzavi Q99465 influenzavi Q9465 influenzavi Q9465 influenzavi Q9465 influenzavi Q9465 influenzavi Q9465 influenzavi Q9465 influenzavi Q98azxi influenza c Q8azxi influenza c
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Submitted (ULL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AY048539; AAL13140.1; -.
EMBL, AY048539; C.membrane; IEA.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
Pfam; PF02480; Herpes_GB; 1.
SEQUENCE 532 AA; 59087 MW; 567D44D52600B76B CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
US8.
Macropodid herpesvirus 1.
Macropodid herpesvirus 1.
Alphaherpesvirinae; Simplexvirus.
NCBI_TAXID=137443;
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Q9FHK6
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q9LQ87
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Q9RYW7
Q9SYW7
Q91PA0
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hevein-like protein HLPf (Fragment).
Sambucus nigra (European elder).
Sukaryota; Viridiplantae; Streeptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; asterids; campanulids; Dipsacales; Adoxaceae; Sambucus.
NCBL_TaxID=4202;
                                                                                                                                                                                                                                                                                                                    "A new antigen receptor gene family that undergoes rearrangement and extensive somatic diversification in sharks.";
Nature 374:168-173(1995).
EMBL; U18701; AAD848195.1; -.
EMBL; U18701; AAD848195.1; -.
HSSP; P01842; ZMCG.
GO; GO:0004872; P:receptor activity; IEA.
InterPro; IPR003101; Ig-11ke.
InterPro; IPR003106; Ig-11ke.
InterPro; IPR00306; Ig-MHC.
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A WEDLINE=9214486; PubMed=10198114;
A WEDLINE=92214486; PubMed=10198114;
A WEDLINE=92214486; PubMed=10198114;
A MATTINE JC.C., Rouge P., Van Leuven F., Does M., Peumans W.J.;
A gene encoding a heveln-like proctein from elderberry fruits is nomologous to PR-4 and class V chitinase genes.";
L Plant Bhygaliol. 1915.457-1556(1999).
R RSP; PO2877; IHEV.
R GO; GO:000861; F:chitin binding; IEA.
R GO; GO:000861; F:chitinase activity; IEA.
R GO; GO:000603; P:chitinase activity; IEA.
R GO; GO:000603; P:chitin catabolism; IEA.
R GO; GO:000603; P:chitin binding IEA.
R GO; GO:0000601; Chitin binding I.
R InterPro; IPR001002; Chitin binding I.
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Novel autigen receptor precupers
Ginglymostoma cirratum (Nurse shark).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii, Galeomorphii; Galeoidea; Orectolobiformes;
Ginglymostomatidee; Ginglymostoma.
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MEDLINE-SS183140; PubMed-7877689;
Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C., Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 54; DB 13; Length 684;
Pred: No. 5.5;
1; Mismatches 8; Indels
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NOVEL ANTIGEN RECEPTOR.
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SMART; SMO0407; IGCl; 4.
PROSITE; PSO835; IG_LIKE; 6.
PROSITE; PSO0290; IG_MHC; 3.
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Best Local Similarity 57.1%;
Matches 12; Conservative
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Bukaryochyta; Uridiglantes, Streptophyta; Embryophyta; Uridiglantes, Streptophyta; Espermatophyta; Magnoliophyta; endicoryledons; core eudicots; asterids; campanulids; Dipascales; Adoxacee; Sambucus.
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MEDLINE=9914486; PubMed=10198114;

Van Damme E.J.M., Charels D., Roy S., Tierens K., Barre A.,

Amtins J.C., Rouge P., Van Leuven F., Does M., Peumans W.J.;

"A gene encoding a hevein-like protein from elderberry fruits is homologous to PR-4 and class V chitinase genes.";

In homologous to PR-4 and class V chitinase genes.";

Plant Physiol. 119:1547-1556(1999).

R HSSP, PO2877; JHBV.

R GO: GO:0006061; F:chitin binding; IEA.

GO: GO:0006061; F:chitin binding; IEA.

GO: GO:0006061; P:chitin catabolism; IEA.

GO: GO:000603; P:chitin catabolism; IEA.

GO: GO:000603; P:chitin catabolism; IEA.

GO: GO:000603; P:chitin catabolism; IEA.

R GO: GO:000603; P:chitin binding_1:

R InterPro; IPRO0102; Chitin binding_1:

R Probom; PRO0187; Chitin binding_1:

R Probom; PRO0187; Chitin binding_1:

R Probom; PRO0180; Glyco hydro 19;

R Probom; PD554900; Glyco hydro 19;

R PRADAT; SM0270; Chitin binding_1:

R PRADATE SM0270; Chitin binding_1:

R PRADATE SM0270; Chitin binding_1:

R PRADATE SM0270; CHITIN BINDER SM0270; CHIT
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Pfam; PF00187; Chitin bind_1; 1.
Propon; PF001087; Glyco Kydzo_19; 1.
Probom; PD00609; Chitin binding_1:
Probom; PD354900; Glyco_Kydzo_19; 1.
PROSITE; SM002774; CHTINA_EN_E 19; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
Chitin-binding.
NON TER
SEQUENCE 333 AA; 37047 MW; 3913256EBC3577B9 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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Q9SYS4
ID Q9SY
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142 ELRESRITDPHLPRS 156
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                                        Similarity
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                    Query Match
Best Local S
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                                                           Matches
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Q9LQ87
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                                                                                                      Sambucus nigra (Buropean elder).
Bukaryophyta; Tracheophyta; Bwbryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Dipascales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                 MEDINE-921486; PubMed=10198114;

MEDINE-921486; PubMed=10198114;

Van Damme E.J.M., Charels D., Roy S., Tierens K., Barre A.,

Van Damme E.J.M., Charels D., Roy S., Tierens K., Barre A.,

Martins J.C., Rouge P., Van Leuven F., Does W., Peumans W.J.;

T. A gene encoding a hevein-like protein from elderberry fruits is homologous to PR-4 and class V chitinase genes.";

Pant Physiol. 119:147-1556(1999).

EMBL; AR074387; AAD11408.1; -.

R HSSP; PO2877; 1HEV.

R GO; GO:0008661; F:chitin binding; IEA.

R GO; GO:0004568; F:chitin binding; IEA.

R GO; GO:0006632; P:chitin catabolism; IEA.

R GO; GO:0006632; P:chitin catabolism; IEA.

R GO; GO:0006632; P:chitin binding_1.

R DI GENEY; IPRO0102; Chitin binding_1.

R PERP: PRO0187; Chitin binding_1.

R PERP: PRO0187; Chitin binding_1; 1.

R PERP: PRO0187; Chitin binding_1; 1.

R PRODOM; PD000609; Chitin binding_1; 1.

R PRODOM; PD000609; Chitin binding_1; 1.

R PRODOM; PD000609; Chitin binding_1; 1.

R RMART; SMORTO: Chitin binding_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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Planctomycetaceae, Pirellula.
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Hypothetical protein; Complete proteome.
SEQUENCE 505 AA; 54499 MW; 9041B06455C20C6F CRC64;
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PROSITE; PS00066; CHITIN_BINDING; 1.
Chitin-binding.
SEQUENCE 333 AA; 37126 MW; 3231BD42F4352CES CRC64;
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Last annotation update)
                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CAT-2003 (TrEMBLrel. 25, Last annotation update)
Hevein-like protein.
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Pred. No. 3.1;
2; Mismatches
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25,
25,
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Best Local Similarity 42.9
Matches 15; Conservative
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01-OCT-2003 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Hypothetical protein.
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Con STRAIN=cv. Columbia;

Liu S., Chan A., Yu G., Lee J., Lenz C., Pham P., Sakano H.,

Liu S., Chan A., Yu G., Lee J., Choi E., Chung M., Gonzalez A.,

Toriumi M., Chin C., Chiou J., Choi E., Chung M., Gonzalez A.,

Howng B., Liu A., Vaysberg M., Altafi H., Brooks S., Buehler E.,

A. Con L., Connay A., Hansen N., Johnson C., Khan S.,

Kim C., Lam B., Miranda M., Nguyen M., Palm C., Shinn P.,

Southwick A., Davis R., Ecker J., Federspiel N., Theologis A.;

Southwick A., Davis R., Ecker J., Federspiel N., Theologis A.;

The sequence of BAC TiN6 from Arabidopsis thaliana chromosome 1.";

Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

BRBL; AC009273; AAF78401.1;

CO, GO:0016531; Fiacyl-CoA thioesterase activity; IEA.

GO; GO:0016531; Fiacyl-CoA metabolism; IEA.

InterPro; IPR003703; Acyl-CoA thio.

R GO; GO:0016531; Acyl-CoA thio.

R Fam; PF02511; Acyl-CoA thio.
                                                                   Gaps
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STRAIN=cv. Columbia;
Seki M., Iida K., Satcu M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enjuh A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Pred. No. 5.2;
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01-UND-2003 (TrEMBLrel. 24, Last annotation update)
Putative acyl Coa thioesterase (At1g01710).
AT1G01710/TIN6_21.
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Last annotation update)
   DB 16;
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                                                                      2; Mismatches
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37.9%; Score 53; 1
50.0%; Pred. No. 5
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Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                         477 GRATOSRIVDPSMPTAPARSTT 498
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                                                                                SEQUENCE FROM N.A.

SHOID P., Chen H., Cheuk R., Kim C.J., Bowser L., Carninci P., Chan M.N., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Landy C.H., Dale J.M., Hayashizaki Y., Hsuan V.W., Lin J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lian B., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S., La Palm C.J., Quach H.L., Sakurai T., Satou M., Soki M., Southwick A., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Subinted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BT005354; AA063418.1; -

EMBL; BT005354; AA063418.1; -

EMBL; BT005354; AA063418.1; -

EMBL; BT005354; AA063418.1; -

EMBL; BT00537; P:acyl-CoA thiocesterase activity; IEA.

GO; GO:0006637; P:acyl-CoA thio.

InterPro; IPR003703; Acyl-CoA thio.

EMBL; PF02551; Acyl-CoA thio;

Pfam; PF02551; Acyl-CoA thio;

Pfam; PF02551; Acyl-CoA thio;

Pfam; PF02551; Acyl-CoA thio;

RRRR, SMRT; SM0100; COMP; Dinding.

Pfam; PF00527; CMP Dinding.

RRRR, SMRT; SM0100; CMP; Dinding.
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"A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
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STRAINS=A3(2) / M145;
MEDLINE=21996410; PubMed=12000953;
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
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SCO1190 OR SCG11A.21C.
Streptomyces coelicolor.
Streptomyces coelicolor.
Bacteria, Actinobacteria, Actinobacteridae, Actinomycetales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.1%; Score 52; DB 10; Length 427; 60.0%; Pred. No. 7;
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Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
"Arabidopsis thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oliver K., Harris D.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NMP_BINDING 3; 1.
48129 MW; 3254604D94333466 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS; TIGRO0189; te
PROSITE; PS50042; CNMP
SEQUENCE 427 AA; 481
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1098AJY0
AC 0098AJY0
DT 01-M

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Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Dipaacales; Adoxacees; Sambucus.
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                                                                                                                                                                                                                                                                                                                                                                                         Nature 417:141-147;
Nature
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murbhy L., Oliver K., O'Neil S., Rabbinowitsch B., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K. Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
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Van Damme E.J.M., Charels D., Roy S., Tierens K., Barre A.,
Wartins G.C., Rouge P., Van Leuver F., Does M., Peumans W.J.;
Martins G.C., Rouge P., Van Leuver F., Does M., Peumans W.J.;
homologous to pR-4 and class V chitinase genes.";
EMBL; AF074386; AAD11407.1;
ESSP; PO2877; IHEV.
                                                                                                                                                                                                                                                                                                                   "Complete genome sequence of the model actinomycete Streptomyces coelicolor {\rm A3}\,(2) .";
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R GO: GO:0004568; Fichtinase activity; IEA.

R GO: GO:0016998; P:collinase activity; IEA.

R GO: GO:0016998; P:collinase activity; IEA.

R GO: GO:0006032; P:chtin catabolism; IEA.

R GO: GO:000051; P:creponse to pest/pathogen/parasite; IEA.

R GO: GO:000051; P:creponse to pest/pathogen/parasite; IEA.

InterPro; IPR001002; Chitin binding 1.

R ProDom; PR01018; Glyco hydro 19.

R ProDom; P01018; Chitin binding 1.

R ProDom; P01018; Chitin binding 1.

R PR05ITE; P800774; CHITINASE 19.2; 1.

R PR05ITE; P800026; CHITIN BINDING; 1.

R PR05ITE; P800026; CHITIN BINDING; 1.

R ERQUENCE 333 AA; 36922 MW; 70C6969392A1174A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.1%; Score 52; DB 16; Length 533; 58.8%; Pred. No. 8.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane, Complete proteome.
SEQUENCE 533 AA; 54474 MW; 49C650E9797FEF77 CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                             Hopwood D.A.;
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1092760
AC 092760
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-CC
DE Hevei,
DE Hevei,
DE Campa
CC Sperm

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Gaps

14;

4; Mismatches Score 50; Pred. No.

DB 12; Length 1103; 6; Indels

us-09-701-623c-5.rspt

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35.7%;
36.8%;
  Query Match
Best Local Similarity 36.8
Matches 14; Conservative
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01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
                                                                                                                GETYQS - - - - RVT
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Q91PA8
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MEDLINE=21395181; PubMed=11504428;
Zhu H., Hong J., Ye R., Chen J., Yu S., Adams M.J.;
Sequence analysis shows that Ribgrass mosaic virus Shanghai isolate (RMV-Sh) is closely related to Youcai mosaic virus.";
Arch. Virol. 146:1231-1238(2001).
                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ribgrass mosaic virus (RMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
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Crucifer tobamovirus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
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A Zhu H., Hong J., Chen J., Yu S.,
Zhu H., Hong J., Chen J.,
Zhu H., Hong J., Chen J.,
Zhu H., Hong J., Chen J.,
Zhu H., Hong J., Land J., Land J.,
Zhu Go, Go:0003174; F:RNA helicase activity, IEA.
Zhu Go; Go:000316; F:RNA helicase activity, IEA.
Zhu Go; Go:0005396; F:RNA processing; IEA.
Zhu Go; Go:0005396; P:RNA processing; IEA.
Zhu Go; Go:0005396; Zhu And J., Zhu J.,
Zhu J., Zhu J., Zhu J., Zhu J.,
Zhu J., Zhu J., Zhu J.,
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Zhu J., Zhu J., Zhu J.
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                                                             15;
        Length 333;
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                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Ryabov E.V., Walsh J.;
"Infectious cDNA clone of Crucifer tobamovirus.";
Submitted (JUN-2010) to the EMBL/GenBank/DDBJ databases.
EMBL; AY31886; AAP79444.1; -.
SEQUENCE 1103 AA; 124693 MW; 187B172584921A07 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1031 GETYEKTAIVRITATPLEIISRASPHVLVALTRHTTRC 1068
                                                                                                                                                                                                                                                                                                                                          091PA7;
0-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last sequence update)
Last annotation update)
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Score 50.5; DB 10;
Pred. No. 9.4;
3; Mismatches 3;
                                                                                                                   22
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                                                                                                                                                      --SRVTHPHLPRALMRST
                                                                                                                                                                                                                                                                                                                  1103 AA.
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                                                                                                                                                                                                                                                                                                               PRT;
        36.1%;
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                                                                14; Conservative
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                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA replicase component
                             Best Local Similarity
Matches 14; Conserv
                                                                                                                        1 CGETYQ----
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              Query Match
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Matches
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1091PA7
1091PA7
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1091PA 1091PA 1091PA 1091PA 1091PA 1091PA 1091PA 1091PA 109PA 109P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=94341372; PubMed=7545946;
Dorokhov Y.L., Ivanov P.A., Novikov V.K., Agranovsky A.A., Morozov S., Efimov V.A., Camper R., Atabekov J.G.;
"Complete nucleotide sequence and genome organization of a tobamovirus infecting cruciferae plants.";
FEBS Lett. 350:5-8(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dorokhov Y.L., Ivanov P.A., Novikov V.K., Efimov V.A., Atabekov I.G., Efimov V.A., Casper R., Atabekov J.G.; Cabamovirus of the Cruciferae family: nucleotide sequence of the 5'-untranslated region and nonstructural protein genes controlling replication viral genome.", Dokl. Akad. Nauk SSSR 335:792-798(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Tobacco mosaic virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
NCBI_TaxID=12242;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mosaic virus.";

Mol. Biol. (Mosk.) 0:0-0(0).

E EMBL, Z29370; CAA82558.1;

R GO; GO:0003724; F:RNA methyltransferase activity; IEA.

GO; GO:0003724; F:RNA methyltransferase activity; IEA.

GO; GO:0003726; F:RNA methyltransferase activity; IEA.

R GO; GO:000396; F:RNA directed RNA polymerase activity; IEA.

R GO; GO:000396; F:RNA processing; IEA.

R GO; GO:0013079; P:RNA processing; IEA.

R InterPro; IPR00260; Viral helicasel.

R InterPro; IPR002588; V methyltransf.

R Ffam; PF01443; Viral helicasel; 1.

R Pfam; FF01660; Vmethyltransf; 1.

R Pfam; FF01660; Vmethyltransf; 1.
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                                                              1031 GETYEKTAIVRLTATPLEIISRASPHVLVALTRHTTRC 1068
                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
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------HPHLPRALMRSTTKC
                                                                                                                                                                                                                                          PRT; 1107 AA
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              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
RNA replicase read-through component.
Ribgrass mosaic virus (RMV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
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Crucifer tobamovirus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Tobamovirus.
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R GO; GO:0005509; F:calcium ion binding; IRA.

GO; GO:0003724; F:mRNA methyltransferase activity; IEA.

GO; GO:0003724; F:mRNA helicase activity; IEA.

GO; GO:0003729; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:000596; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0006350; F:RNA-directed RNA polymerase activity; IEA.

GO; GO:0006350; P:RNA pocessing; IEA.

GO; GO:0006350; P:RNA pocessing; IEA.

GO; GO:0006350; P:RNA pocessing; IEA.

R InterPro; IPR001094; RNA dep.RNApol2.

R InterPro; IPR007094; RNA pol_DS_PS.

R InterPro; IPR007094; RNA pol_DS_PS.

R InterPro; IPR005588; V methyltransf.

R Pfam; PF00443; Viral helicase1; 1.

R Pfam; PF00443; Viral helicase1; 1.
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35.7%; Score 50; DB 12; Length 1597;
Best Local Similarity 36.8%; Pred. No. 58;
Matches 14; Conservative 4; Mismatches 6; Indels 14
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Ryabov E.V., Walsh J.;
"Infectious cDNA clone of Crucifer tobamovirus.";
"Infectious cDNA clone of EMBL/GenBank/DDBJ databases.
SUbmitrad (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY318866; AAP79445.1;
SEQUENCE 1597 AA; 181405 WW; AEB67B7779AF1807 CRC64;
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SEQUENCE 1597 AA, 181462 MW; 9E6576FF595E0DEF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Shanghai;
Zhu H., Hong J., Chen J., Yu S.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
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PRT; 1597 AA
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Gaps

6; Indels 14;

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2 GETYQS----RVT------HPHLPRALMRSTIKC 25
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completed: February 26, 2004, 08:27:10 ne : 35.4 secs Search cor Job time

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TYPE: PRT
ORGANISM: Human
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US-10-076-674-10
Query Match
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/ cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.ppp:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
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1 US-10-35-161A-10

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3 US-10-152-190-6

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TYPE: PRT
CRGANISM: Human CH3
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US-10-152-190-4
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Publication No. US20040009897A1
| GENERAL INFORMATION:
| APPLICANT: SOKOL1, Kenneth K.
| TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
| TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
| TITLE OF INVENTION: UNBER: US/10/355,161A
| CURRENT FILING DATE: 2003-01-31
| PRIOR PELICATION NUMBER: US/10/076674
| PRIOR FILING DATE: 2002-02-14
| NUMBER OF SEQ ID NOS: 13
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 11
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US-10-076-674-11
US-10-076-674-11
Sequence 11, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
APPLICANT: SOKOll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REPERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 11
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Best Local Similarity 100.0%; Pred. No. 5.8e-13;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 140; DB 15;
Best Local Similarity 100.0%; Pred. No. 5.7e-13;
Matches 25; Conservative 0; Mismatches 0;

; LOCATION: (20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-11

                                                                                                                                                                                                                                                                                       ; LOCATION: (19)...(19)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-10
FILE REPERENCE: Immunogen Delivery System CURRENT APPLICATION NUMBER: US/10/355,161A PRIOR APPLICATION NUMBER: US/07/6574 PRIOR PILIOR DATE: 2002-01-14 PRIOR FILING DATE: 2002-02-14 NUMBER OF SEQ ID NOS: 13 SOFTWARE: Patentin version 3:1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 CGETYQSRVTHPHLPRALMRSTTKC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGETYQSRVTHPHLPRALMRSTTKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 CGETYQSRVTHPHLPRALMRSTTKC 44
                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
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ORGANISM: Human
                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Human
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US-10-355-161A-11
                                                                                                                                                      SEQ ID NO 10
LENGTH: 44
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                                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/10152190
Publication No. US2030096369A1
GENERAL INFORMATION:
APPLICANT: Morsey, Mohamad A.
TITLE OF INVENTION:
FILE REFERENCE: PC11011A
CURRENT APPLICATION NUMBER: US/10/152,190
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
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                                                                                                                              Length 45;
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                                                                                                                            Query Match 100.0%; Score 140; DB 15; Best Local Similarity 100.0%; Pred. No. 5.8e-13; Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
83.6%; Score 117; DB 14;
Best Local Similarity 95.7%; Pred. No. 3.1e-09;
Matches 22; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT; ORGANISM: Baculovirus expressed human CH3 domain US-10-152-190-6
ORGANISM: Human
FEATURE:
NAME/KEY: misc feature
DCCATION: (20)..(20)
OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-161A-11
                                                                                                                                                                                                                                 21 CGETYQSRVTHPHLPRALMRSTTKC 45
                                                                                                                                                                                                     1 CGETYOSRVTHPHLPRALMRSTTKC 25
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US-09-809-746-2
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us-09-701-623c-5.rapb

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TYPE: PRT
CRGANISM: Homo sapiens
US-09-847-208-6
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ORGANISM: homo sapiens
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APPLICANT: Garman, Scott Clayton
APPLICANT: Garman, Scott Clayton
APPLICANT: Garman, Scott Clayton
APPLICANT: Wurzburg, Beth A.
APPLICANT: Winzburg, Can Pierre
TITLE OF INVENTION: THREE-DIENSIONAL MODEL OF A COMPLEX BETWEEN A FC
TITLE OF INVENTION: ANTIBODY AND USES THEREOF
TILE REPERENCE: AL-8
CURRENT APPLICATION NUMBER: G0/189,853
FRIOR PILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 222
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Sequence 2, Application US/09809746
Fatent No. US20010039479A1
GENERAL INFORMATION:
APPLICANT: Jardetzky, Theodore S.
APPLICANT: Jardetzky, Theodore S.
TITLE OF INVENTION: TARTE-DIMENSIONAL MODEL OF A FC REGION OF AN 1GE
TITLE OF INVENTION: TARTE-DIMENSIONAL MODEL OF A FC REGION OF AN 1GE
TITLE OF INVENTION: TARTE-DIMENSIONAL MODEL OF A FC REGION OF AN 1GE
TITLE OF INVENTION: AMTER-DIMENSIONAL MODEL OF A FC REGION OF AN 1GE
CURRENT APPLICATION NUMBER: 60/234, 377
PRIOR FILING DATE: 2000-09-22
PRIOR PRING DATE: 2000-09-15
PRIOR FILING DATE: 2000-09-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 83.6%; Score 117; DB 9; Length 222; Best Local Similarity 95.7%; Pred. No. 6.2e-09; Matches 22; Conservative 0; Mismatches 1; Indels
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95.7%; Pred. No. 6.2e-09;
tive 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09809715; Publication No. US20030003502A1; GENERAL INFORMATION:
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Best Local Similarity 95.74
Best Local Similarity
22; Conservative
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CRGANISM: Homo sapiens
US-09-809-715-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
CRGANISM: Homo sapiens
US-09-809-746-2
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US-09-847-208-6
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Gaps
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; Sequence 2, Application US/09949375A
; GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
FILE REPERDICE: 361-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 2.
TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF TITLE OF INVENTION: 1GE-MEDIATED ALLERGIC DISEASES FILE REPERRENCE: UGCJ. 002A.

CURRENT PELLING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 177

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6

LENGTH: 320
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NAME/KEX: DOMAIN
LOCATION: (8)..(103)
OTHER INFORMATION: Human IGE heavy chain C2 domain
FEATURE:
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LOCATION: (100)..(114)
OTHER INFORMATION: Epitope including C2C3 linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE
LOCATION: (210)..(218)
OTHER: PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (212).. (215)
OTHER_INFORMATION: Linker between domains C3
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LOCATION: (112)..(211)
LOCATION: (112)...(211)
OTHER INFORMATION: Human IgE heavy chain C3
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (216)..(317)
OTHER INFORMATION: Human IgE heavy chain C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: MISC FEATURE
LOCATION: (104)..(111)
OTHER INFORMATION: Linker between domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 GETYQCRVTHPHLPRALMRSTTK 208
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OTHER INFORMATION: Epitope in BC loop
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RESULT 15
US-10-176-664-1
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* OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO:
US-09-349-375A-6
                                                                                                                                                  Query Match 83.6%; Score 117; DB 9; Length 323; Best Local Similarity 95.7%; Pred. No. 9.1e-09; Matches 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

83.6%; Score 117; DB 9; Length 323;
Best Local Similarity 95.7%; Pred. No. 9.1e-09;
Matches 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 83.6%; Score 117; DB 9; Length 323; 1 Similarity 95.7%; Pred. No. 9.1e-09; 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/09949375A; Patent No. US20020172673A1; GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE; FILE REFERENCE: 3631-0111P; CURRENT APPLICATION UNDER: US/09/949,375A; CURRENT APPLICATION UNDER: US/09/949,375A; CURRENT FILING DATE: 2002-01-18
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
ILENGTH: 323
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) Sequence 6, Application US/09949375A
; Patent No. US20020172673A1
; GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: NETHOD FOR DOWN-REGULATING IGE
FILE REPERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
; CURRENT FILING BATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentin version 3.1
                     FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1967...(206)
CTHER INFORMATION: Epitope in FG loop
US-09-949-375A-2
OTHER INFORMATION: Epitope in DE loop
                                                                                                                                                                                                                                                                              189 GETYQCRVTHPHLPRALMRSTTK 211
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 22; Conserv
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LENGTH: 323
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189 GETYÖCRVTHPHLPRALMRSTTK 211

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; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO:
US-09-949-375A-10
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83.6%; Score 117; DB 9; Length 331;
Best Local Similarity 95.7%; Pred. No. 9.3e-09;
Matches 22; Conservative 0; Mismatches 1; Indels
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US-09-949-375A-10
US-09-949-375A-10
Sequence 10, Application US/09949375A
Patent No. UG20020172673A1
GENERAL INFORMATION:
APPLICANT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFUMARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 330
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ORGANIGM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Synthetically generated proteins
US-09-401-636-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

83.6%; Score 117; DB 9;
Best Local Similarity 95.7%; Pred. No. 9.3e-09;
Matches 22; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09401636
Patent No. US20010038843A1
GENERAL INFORMATION:
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFRENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FASEESE for Windows Version 4.0
SEQ ID NO 1
LENGTH: 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/10176664
Publication No. US20030031663A1
Publication No. US20030031663A1
APPLICANT: Hellman, Lars T.
TILE OF INVENTION: BENBANCED VACCINES
FILE REPERENCE: 10223/006001
CURRENT PILION DAMBER: US/10/176,664
CURRENT PILION DATE: 2022-06-19
PRIOR PILING DATE: 1999-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 GETYQCRVTHPHLPRALMRSTTK 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 GETYQCRVTHPHLPRALMRSTTK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GETYQSRVTHPHLPRALMRSTTK 24
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                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
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0;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein February 26, 2004, 08:18:56; Search time 10 Seconds (without alignments) 240.479 Million cell updates/sec Run on:

US-09-701-623C-6 141 1 CGETYYSRVTHPHLPKDIVRSIAKC 25 score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched: 283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

		di			SUMMARIES	
Result No.	Score	Query Match	Length	DB	di	Description
	888	62.4	426	~	I36948	Ig epsilon-chain
8	60	0	428	Н	ЕННО	g epsi
e	82	58.2	429	Н	EHRT	ប
4	58	41.1	107	N	I68730	gE chain C3
Ŋ	58	41.1	107	N	168726	Ö
φ	58	41.1	388	Н	EHIMS	epsilon ch
7	58	41.1	548	~	S38864	Ig epsilon chain C
œ	54	38.3	116	N	837909	
σ		38.3	394	C)	T19571	
10		38.3	1306	01	842659	æ
11		38.3	1625		T02921	
12	54	38.3	2311		T06161	
13	54	38.3	2325	Ŋ	T02235	acetyl-CoA carboxy
14	52	36.9	1756		T02599	hypothetical prote
15	51.5	36.5	605		FPMS	alpha-fetoprotein
16	51	36.2	106		A03859	hypothetical prote
17	51	36.2	195		A75171	hypothetical prote
18	20	35.5	539		T48197	hypothetical prote
19	٠	'n.	381		S28115	gas-vesicle protei
20	٠	35.1	382		JQ1122	
21	49.5	35.1	382		T08243	gas-vesicle operon
22	4.0	34.8	684	N	860266	novel antigen rece
23		34.8	1095	7	C59437	KIAA0456 protein [
24	4.0	34.8	1685	7	T02750	acetyl-CoA carboxy
25		34.0	367	7	D97096	probable permease,
26	48	34.0	384	7	T06814	-binding
27	48	34.0	454	7	A46532	Ig mu chain C regi
28	48	34.0	958	7	1556	protein
29	4.8	34.0	1161	7	S18738	protein

Ig upsilon chain -	hypothetical prote	molybdenum transpo	probable GTP-bindi	GTP-binding regula	protein T6D22.14 [acetyl-CoA carboxy	probable phosphoes	conserved hypothet	hypothetical prote	hypothetical prote	Ħ	H-2 class II histo	iis	probable membrane	Ig heavy chain pre
843147	C86148	AE0595	T16971	RGTOOA	D86215	T09538	C97419	AD2637	T48376	B71044	155951	A60497	\$10989	T34940	S04845
7	7	~	7	н	N	N	Н	N	0	N	N	N	ď	~	N
110	320	352	372	384	2254	2257	242	242	248	198	245	264	264	382	549
33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.0	33.0	33.0	32.6	32.6	32.6	32.6	32.6	32.6
47	47	47	47	47	47	47	46.5	46.5	46.5	46	46	46	46	46	46
000	31	22	33	3.4	35	36	3.7	38	6	9	ᅼ	12	43	14	45

ALIGNMENTS

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Ig opsilon-chain - chimpanzee (fragment)
C_Species: Pan troglodytes (chimpanzee)
C_Species: Pan troglodytes (chimpanzee)
C_Species: Pan troglodytes (chimpanzee)
C_SAccession: 136948
R_Sakoyama, Y.: Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A;Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangut: A;Reference number: 136948; MUID:87147196; PMID:3103123
A;Accession: 136948
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-426 cRES.
A;Residues: 1-426 cRES.
A;Cross-references: GB:MIS398; NID:g176797; PIDN:AAA35416.1; PID:g176798
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0
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;336-405/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
62.4%; Score 88; DB 2; I
Best Local Similarity 69.6%; Pred. No. 4.8e-05;
Matches 16; Conservative 2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 GETYQCRVTHPHLPRALVRSTTK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GETYYSRVTHPHLPKDIVRSIAK 24
RESULT 1
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Ignorian chain C region - human.

C;Species: Homo sapiens (man)
C;Date: 31-Mar-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C4
R;Flanagan, J.G.; Rabbitts, T.H.
A;Flanagan, J.G.; Rabbitts, MUID:84236029; PMID:6234164

A;Accession: A22771
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-428 <FILA>
A;Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
B;Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
BMBO J. 1, 1539-1544, 1982
A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudo
A;Reference number: A23195; MUID:84207910; PMID:6327276
A;Accession: A23195

A; Molecule type: DNA A; Residues 2-428 «UED> A; Cress-references: GB: J00222; NID: 9184755 R; Zhang, K.; Saxon, A.; Max, E.E.

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A,Molecule type: mRNA
A,Residues: 1-429 cHEL>
A,Experimental source: strain LOU/c/Wsl, immunocytoma IR2
A,Experimental source: strain LOU/c/Wsl, immunocytoma IR2
R,Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.
BNA 1, 335-343, 1982
A,Title: A cloned cDNA probe for rat immunoglobulin epsilon heavy chain: construction, A,Teference number: A90937; MUID:83182019; PMID:6820340
A,Contents: myeloma IR162
A,Contents: myeloma IR162
A,Contents: myeloma IR162
A,Molecule type: mRNA
A,Residues: 'N',169-307, 'L',309-342 cKIN>
C,Complex: An immunoglobulin heterotetramer subunit consists of two identical light (Ka iain disulfide bonds: In some cases, such as IGA and IGM, the subunits associate into I c,Superfamily: immunoglobulin c region; immunoglobulin homology clM2>
F,118-186/Domain: immunoglobulin homology clM2>
F,123-291/Domain: immunoglobulin homology clM3>
F,223-291/Domain: immunoglobulin homology clM3>
F,246,99,170,246,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Map position: 14632.33-14632.33

A Introns: 1/1, 104/1, 211/1, 319/1

A Introns: 1/1, 104/1, 211/1, 319/1

Complex: An immunoglobulin heteroteramer subunit consists of two identical light (ka) thain disulfide bonds: In some cases, such as IgA and IgM, the subunits associate into I c; Complex: An immunoglobulin c region; immunoglobulin homology

C; Superfamily: immunoglobulin c region; immunoglobulin homology cimis-
F; 228-97/Domain: immunoglobulin homology cimis-
F; 228-195/Domain: immunoglobulin homology cimis-
F; 338-407/Domain: immunoglobulin homology cimis-
F; 338-407/Domain: immunoglobulin homology cimis-
F; 340-25-25/15-35-25/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/15-35/
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Cibate: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 16-Jul-1999
Cibates in: A93442; A9037; A02143
RiHellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nuclaic, Acids Res. 10, 6041-6049, 1982
A;Title: Structure and evolution of the heavy chain from rat immunoglobulin 3A;Reference number: A93442; MUID:83064537; PMID:6292865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                       A;Note: sequence extracted from NCBI backbone (NCBIP:125299)
A;Accession: A46536
A;Accession: A46536
A;Accule type: DNA
A;Residues: 401-428 -HE3>
A;Cross-references: GB:53497; NID:g263162; PIDN:AAB24855.1; PID:g263163
A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIP:123483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .;
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69.6%; Pred. No. 0.00036;
iive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Gene: GDB:1GHE
A, Cross-references: GDB:119335, OMIM:147180
                  source: B cell myeloma U-266
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nes 15; Conservative
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ses 16; Conserv
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Best Local S
Matches 16
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J. Exp. Med. 176, 233-243, 1992
A.Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing A.Reference number: PH1214
M.M.Coession: PH1214
A.M.Coession: PH1214
A.M.Coession: PH1214
A.M.Coession: PH1214
A.M.Coession: PH1214
A.M.Coession: A.M.C. A. Comda, M. D. Saada, R.; Igarashi, K.; Kikuchi, M.; Sugi M.; Corss references: EMBL.K6593, GB.538669; MID:922997
A.Cross references: EMBL.K6593, GB.538669; MID:923997
A.Cross references: EMBL.K6593, GB.538669; MID:938609; M., Sudi M.; Sudi M.; Rickession: A3491; MUD:9316897; PM1D:5300763
A.M.Coession: A3491; MUD:9316897; PM1D:5300763
A.M.Coession: A3491; MUD:9316897; PM1D:5300763
A.M.Coession: A3491; MUD:9316897; PM1D:588269
A.Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A.Reference mumber: A990824; MUD:83001945; PMID:588269
A.M.Coession: B.M.Coession: B.M.C
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FEBS Lett. 224, 306-310, 1987
A;Title: Purification and characterization of a recombinant human IgE FC-epsilon fragmen A;Reference number: S02438; MUID:88083554; PMID:3121387
A;Accession: S02438
A;Accession: S02438
A;Accession: S02438
A;Reference number: so2438; MUID:88083554; PMID:3121387
A;Residues: 98-352 AIRC
A;Residues: 98-352 AIRC
A;Accession: Chem. 269, 456-462, 1994
A;Attle: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A;Accession: A53116
A;Accession: A5410316
A;Accession: A5410316
A;Accession: A5410316
A;Accession: A5410316
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A;Accession: A5410316
A;Accession: A
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A,Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of A,Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of A,Teference number: A46536, MUID:93122085; PMID:8419166

A,Status: preliminary, not compared with conceptual translation
A,Status: preliminary, not compared with conceptual translation
A,Status: mRNA
A,Residues: 382-426 FHEL>
A,Cross-references: GB:855273; NID:9263166; PIDN:AAB24857.1; PID:9263167
A,Cross-reference extracted from NCBI backbone (NCBIP:125297)
A,Accession: D46536
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2 GETYYSRVTHPHLPKDIVRSIAK 24

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hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into li C'Superfamily: immunoglobulin C region; immunoglobulin homology (Exgwands: duplication; glycoprotein; heterotetramer; immunoglobulin processes in the subunit immunoglobulin homology (Ergment) F:81-144/Domain: immunoglobulin homology 
F:81-149/Domain: immunoglobulin homology 
F:290-361/Domain: immunoglobulin homology 
F:290-361/Domain: immunoglobulin homology F:290-361/Domain: immunoglobulin homology F:10,51,62,183;205,228,332,819inding site: carbohydrate (Asn) (covalent) #status pred
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A;Molecule type: DNA
A;Residues: 1-116 <POH>
A;Cossidues: 1-116 <POH>
A;Cross-references: EMBL:228084; NID:g486122; PID:g486123; GSPDB:GN00011; MIPS:YKL084w
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use peailon chain C region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Accession: S38864
R;Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of A;Reference number: S38864
A;Accession: S38864
A;Accession
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C;Species: Saccharomyces cerevisiae
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Dec-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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41.1%; Score 58; DB 1; Length 388; Best Local Similarity 56.5%; Pred. No. 1; Matches 13; Conservative 0; Mismatches 10; Indels
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R;Pohl, T.M.; Pohl, F.M.
submitted to the Protein Sequence Database, March 1994
A;Accession: $37897
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56.5%; Pred. No. 1.5;
ive 0; Mismatches
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Matches 10; Conservative
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Best Local Similarity
Matches 13; Conserva
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession: A02144
R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain CDNA.
A;Reference number: A02144
A;Reference number: A02144
A;Molecule Lype: mRNA
A;Molecule 1-388 <LLU>
A;Residues: 1-388 <LLU>
A;Residues: 1-388 <LLU>
A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
                                                                                                                                                                                                                                           IgE chain C3 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: 168730
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid A;Accession: 168730
A;Accession: 168730
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 168730
A;Status: preliminary; translated from GB/EMBL/DDBJ
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Graceasian C3 region - mouse (fragment)

C;Becles: Mus musculus (house mouse)

C;Accessian: 186726

E;Accessian: 186726

E;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

E;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

E;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

E;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

E;Shinkai, Y.; Nakauchi, T.; Okumura, K.

A;Atitles: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid a;Accession: 168726

E;Atitles: Dinaminary; translated from GB/EMBL/DDBJ

A;Residues: 1-107 <RES-

A;Residues: 1-107 <RES-

A;Cross-references: GS:M22930; NID:g194455; PIDN:AAA37911.1; PID:g194460

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;22-90/Domain: immunoglobulin homology <IMM>
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A;Coss-references: GR12233; NID:g194464; PIDN:AAA37915.1; PID:g194469
A;Cross-references: GB:M22933; NID:g194464; PIDN:AAA37915.1; PID:g194469
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           y Match 41.1%; Score 58; DB 2; Length 107; Local Similarity 56.5%; Pred. No. 0.27; hes 13; Conservative 0; Mismatches 10; Indels
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                                                             284 GEGYQCRVDHPHFPKPIVRSITK 306
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Best Local Similarity 56.5
Matches 13; Conservative
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C;Species: Zea mays (maize)
C;Species: Zea mays (maize)
C;Bate: Z4-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T02921
R;Ashton, A.R.; Jenkins, C.L.D.; Whitfeld, P.R.
Plant Mol. Biol. 24, 35-49, 1994
A;Title: Molecular cloning of two different cDNAs for maize acetyl CoA carboxylase.
A;Reference number: S42659, MUID:94154242; PMID:7906562
A;Accession: T02921
A;Stetus: prelimitary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1625 cASH>
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hypothetical protein C29F7.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T19F71
R;McMurray, A.
Submitted to the EMBL Data Library, March 1997
A;Reference number: Z19144
A;Reference number: Z19144
A;Reference to the EMBL Data Library, March 1997
A;Reference number: Z19144
A;Reference number: D19F71
A;Reference number: D19F71
A;Reference number: D19F71
A;Reference number: Z19144
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

38.3%; Score 54; DB 2; Length 394;

Best Local Similarity 60.0%; Pred. No. 4.1;

Matches 9; Conservative 3; Mismatches 3; Indels
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nes 10; Conservative
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acetyl-CoA carboxylase (EC 6.4.1.2) - wheat
NiAlternate names: acetyl-coenzyme A carboxylase
NiAlternate names: acetyl-coenzyme A carboxylase
Cipecies Triticum aestivum (common wheat)
Cipecies Triticum aestivum (common wheat)
Cipacesion: To6161; T06162; S42660; S78600; S35959
CiAccession: T06161; T06162; S42660; S78600; S35959
CiAccession: T06161; T06162; S42660; S78600; S35959
CiAccession: T06161; T06162; S42660; S78600; S35959
Cipacesion: T06161; T06162; S42660; S78600; S35959
Aighte: Parts, Display (N.S.A.94, 14779-4184, 1997
Aighte: Plastid localized acetyl-CoA carboxylase of bread wheat is encoded by a single AiReference number: Z15495; WUID:98054381; PMID:9391173
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C; Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
C; Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology <BCH>
F; 134-640/Domain: biotin carboxylase homology <BCH>
F; 767-839/Domain: lipoyl/biotin-binding homology <LPB>
F; 806/Binding site: biotin (Lys) (covalent) #status predicted
A;Cross-references: EMBL:224449; NID:g1272684; PIDN:CAA80822.1; PID:g1272685
A;Experimental source: strain B73; leaf
C;Function:
C;Function:
C;Function: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
C;Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biotin
C;Keywords: ligase
F;68-140/Domain: lipoyl/biotin-binding homology <LPB>
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A,Residues: 'WRIYM',1771-2026,'K',2028-2073,'F',2075-2108,'V',2110-2120,'L',2122,'A',21
A,Cross-references: EMBL:Z23038; NID:g396278; PIDN:CRA80573.1; PID:g396279
A,Accession: S78600
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.Residues: 1847-1852,'E',1854-1863;1947-1962,'D',1964;2085-2091,'HL';2139-2155,'I',215
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Introns: 69/1; 90/2; 209/3; 278/3; 332/3; 363/3; 35/3; 453/3; 485/1; 547/3; 564/3;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA,
A;Molecule type: DNA
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A;Molecule type: m2NA
A;Moledues: 1-211 < GONA
A;Residues: 1-211 < GONA
A;Cross-references: EMBL.AF029895; NID:92827149; PIDN:AAC39330.1; PID:92827150
A;Experimental source: cv. Hard Red Winter Tam 107, light-grown seedlings
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Pred. No. 18;
3; Mismatches
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NA1ternate names: hypothetical protein F26C24.9
NA1ternate names: hypothetical protein F26C24.9
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, June 1998
A;Reference number: 2102699
A;Reference number: 2102599
A;Accession: 702599
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C;Keywords: ligase
F;134-640,Domain: blotin carboxylase homology <BCH>
F;134-640,Domain: lipoyl/biotin-binding homology <LPB>
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Local Similarity 55.6%;
es 10; Conservative
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### Solution: 29/1; 46/2; 86/3; 157/2; 201/3; 234/2; 277/3; 349/2; 393/3; 426/2; 472/3; 54 % Thirtons: 29/1; 46/2; 86/3; 157/2; 201/3; 234/2; 277/3; 349/2; 393/3; 426/2; 472/3; 54 % Introns: 29/1; 46/2; 8crum albumin; serum albumin repeat homology (Superfamily: serum albumin; spredicted (SIG) (Signatus) predicted (SIG) (Signatus) serum albumin repeat homology (SA1) (Signatus) serum albumin repeat homology (SA2) (Signatus) serum albumin repeat homology (SA2) (Signatus) serum albumin repeat homology (SA3) (Signatus) (Signatus) serum albumin repeat homology (SA3) (Signatus) (Signatus
alpha-fetoprotein precursor - mouse

NyAlernate names: AFP; alpha-1-fetoprotein precursor; alpha-fetoglobulin precursor

Syspecies: Mus musculus (house mouse)

C;Date: 01-Sep-1981 #sequence revision 28-May-1986 #text_change 12-Jun-1998

C;Accession: A93254; A92305; R03235

Silaw, S.W.; Dugaiczyk, A.

Nature 291, 201-205, 1981

A;Title: Homology between the primary structure of alpha-fetoprotein, deduced from a con A;Reference number: A93254; MUID:81197641; PMID:6164927
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Ajacces-references: GB:V00743
Mol. Biol. Evol. 2, 347-358, 1985
Ajacces-redences: Ajacces-redences revolution of alpha-fetoprotein approaches that of pseudor Ajacces-redences annotation; revision to residue 598, reported in reference A93254 as Glu, should have been reported as Ajacces-redences residue 598, reported in reference A93254 as Glu, should have been reported as Ajacces-redences annotation of alpha-fetoprotein and albumin: I. A comparison of the primary Ajacces-redence number: A92305; MUID:81117287; PMID:6161929
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A;Contents: annotation; exon-intron junctions
C;Comment: Mouse APP has two carbohydrate chains and was found to bind estrogens and
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A;Residues: 15-532,'RAKL',538-605 <GOR>
A;Cross-references: GB:M16381
A;Note: the beginning of the mature protein was placed at residue :
R;Eiferman, F.A; Young, P.R.; Scott, R.W.; Tilghman, S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 605;
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1; Conservative
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GenCore version 5.1.6
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- protein search, using sw model OM protein February 26, 2004, 08:17:40; Search time 6.4 Seconds (without alignments) 203.399 Million cell updates/sec Run on:

141 1 CGETYYSRVTHPHLPKDIVRSIAKC 25 US-09-701-623C-6 score:

Scoring table: Sequence:

141681 segs, 52070155 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 141681

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	iption	P01854 homo sapien	55 rattl	P06336 mus musculu	P36078 saccharomyc	2 mus mu		_		4			Q7mt94 porphyromon							Q57957 methanococc	_	influenz	xenoi		mus n			P35570 rattus norv	Q8e6rl streptococc		halo	043791 homo sapien	38 baci	Q9zuu0 arabidopsis
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ALIGNMENTS

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SEQUENCE FROM N.A., AND VARIANT LEU-359.
MEDLINE-83001945; PubMed-6288268;
MAX E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
"Duplication and deletion in the human immunoglobulin epsilon genes.";
Cell 29:691-699(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [5]
PRELIMINARY SEQUENCE (MYELOWA PROTEIN ND).
Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
Rennich H.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36,
Marcel Dekker, New York (1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=84236029; PubMed=6234164;
Flanagan J.G., Rabbitts T.H.;
"The sequence of a human immunoglobulin epsilon heavy chain constant region gene, and evidence for three non-allelic genes.";
EMBO J. 1:655-660(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDILINE-8816897; Pubmed=6300763;
MEDILINE-8816897; Pubmed=6300763;
Seno M., Kurokswa T., Ono Y., Onda H., Sasada R., Igarashi K.,
Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
"Molecular cloning and nucleotide sequencing of human immunoglobulin
epsilon chain cDNa ";
Nucleic Acids Res. 11:719-726(1983).
                                                                                                                                                                                                                                                                           Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCB_TaxID=9606;
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MEDLINE=83065234; PubMed=6815656;
Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney is Bell L.O., Gould H.J.,
"Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Froc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

MEDLINE-84207910; PubMed=6327276;
Uded S., Nakai S., Nishida Y., Hisajima H., Honjo T.;
"Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudogene that lacks introns.";
EMBO J. 1:1539-1544 (1982).
                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
1g epsilon chain C region.
428 AA.
PRT;
STANDARD;
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       HUMAN
                                           BRITER REPRESENTATION OF STANFORM STANF
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SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
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Nucleic Acids Res. 10:6041-6049(1982).
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Best Local Similarity 65.2
Matches 15; Conservative
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                                                                                                                                                                                     GO, GO:000823; F:antigen binding; NAS.
GO; GO:000823; F:antigen binding; NAS.
GO; GO:000855; P:immune response; NAS.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003006; Ig_MHC.
FEAM; PR00047; Ig; 4.
SMART; SM00407; IGc1; 4.
PROSTIE; PS50835; IG_LIKE; 4.
PROSTIE; PS00229; IG_MHC; 3.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
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M -> L (POSSIBLE POLYMORPHISM).
/FIId=VAR_003885.
                                                                                                                                                                                                                                                                                     IG-LIKE 1.
IG-LIKE 2.
IG-LIKE 3.
IG-LIKE 4.
INTERCHAIN (WITH A LIGHT CHAIN).
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3D-STRUCTURE MODELING.
MEDLINE=87089848; PubMed=3796618;
Padlan B.A., Davies D.R.;
"A model of the Fc of immunoglobulin E.";
MO1. Immunol. 23:1063-1075(1986).
-!- SIMILARITY: Contains 4 immunoglobulin-like domains.
                                                                                                          EMBL, L00022; AABS9424.1; ALT_INIT.
PTR; A22771; BHU.
PDB; 11GE; 12-JUL-92.
PDB; 1694; 16-MAY-01.
PDB; 100V; 18-SEP-02.
GGREW; HGNC:522; IGHE.
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DISULFID 14
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Gaps
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                                   60.3%; Score 85; DB 1; Length 428; 65.2%; Pred. No. 4.4e-05; ive 3; Mismatches 5; Indels
47019 MW; 25C4CA072AA558A0 CRC64;
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21-UTL-1986 (Rel. 01, Created)
21-UTL-1986 (Rel. 01, Last sequence update)
21-UTL-1986 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
11 epsilon chain C region.
Rattus norvegicus (Rat).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCB1_TaxID=10116; 429 AA.

STRAIN=LOU/C/WSL,

BEDLINE=83064537, PubMed=6292865,
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
"Structure and evolution of the heavy chain from rat immunoglobulin SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
MEDLINE=83182019; PubMed=6820340;
Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.,;
"A clonde CDNA probe for rat immunoglobulin epsilon heavy chain:
construction, identification, and DNA sequence.";
DNA 1:335-343(1982).

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421 AA;
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                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FMHL utstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=84236092; PubMed=6329728;
Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
The nucleotide sequence of the mouse immunoglobulin epsilon gene:
comparison with the human epsilon gene sequence.";
EMBO J. 1:1117-1123(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPC_MOUSE STANDARD; PRT; 421 AA.
P06336; P01856;
21-UUL-1996 (Rel. 01, Created)
01-FRB-1996 (Rel. 33, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38, Last annotation update)
Mus musculus (Mouse).
Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                            "Characterization and molecular cloning of the mRNA for the heavy (epsilon) chain of rat immunoglobulin E.", Proc. Natl. Acad. Sci. U.S. A. 79:1264-1268(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 34-421 FROM N.A.
MEDLINE-83117774; PubMed-6818553;
Liu F.-T., Albrandt K., Sutcliffe J.G., Katz D.H.;
"Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.";
Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
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Pred. No. 0.00012;
0; Mismatches 7; Indels
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IG-LIKE 3.

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IG-LIKE 4.

R -> N (IN REP. 2).

P -> L (IN REP. 2).

W; D2970B34EF8A72B0 CRC64;
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Submitted (APR-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogiobulin domai\overline{\mathbf{n}}_i Immunoglobulin C region; Repeat. NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
   L., Pettersson U., Bennich H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 ĠĠĠŶQCŔŸDĤPĤFPKPÍVŘŠITK 306
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                                                                                                                                                                                                                                                                                                                                                                                               EMBL; J00744; AAA41379.1; ALT_INIT.
PIR; A93442; EHRT.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; Ig; 4.
SMART; SM00407; IG; 4.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
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nes 16; Conservative
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Hypothetical 13.6 kDa protein in MDHI-VMAS intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41.1%; Score 58; DB 1; Length 421; 56.5%; Pred. No. 0.43;
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Pohl T.M., Pohl F.M.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
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PIR; A02144; EHMS.
PIR; A02145; EHMS.
HSSP; P01854; IIGE.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003606; Ig_MHC.
Pfam; PF00047; ig; 4.
Pfam; PR00407; ig; 4.
PROSITE; PS00855; IG_LIKE; 4.
PROSITE; PS00890; IG_MHC; 3.
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NON TER 1 1 90
DOMAIN 91 197
DOMAIN 198 304
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SEQUENCE FROM N.A.

STRAIN=C57BL/6J; TISSUE=Liver;

X RADLINE=21085660; PubMed=11217851;

X RAWAI J., Shinagawa A., Shinadata K., Yoshino M., Itoh M., Ishii Y.,

A Arakawa T., Hara A., Pukunishi Y., Xonno H., Adachi J., Fukuda S.,

A Arawa K., Izawa M., Nishi K., Kiyoswa H., Kondo S., Yamanaka I.,

A Atawa K., Izawa M., Nishi K., Kiyoswa H., Kaukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Kuchl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

Sakai K., Okido T., Furuno M., Ano H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fulita M., Gaziboldi M.,

Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.
MEDLINE=81197641; PubMed=6164927;
Law S.W., Dugaiczyk A.;
"Homology between the primary structure of alpha-fetoprotein, deduced
from a complete cDNA sequence, and serum albumin.";
Nature 291:201-205(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minghetti P.P., Law S.W., Dugaiczyk A.;
"The rate of molecular evolution of alpha-fetoprotein approaches that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                 6
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Best Local Similarity 52.6%; Pred. No. 0.44;
Matches 10; Conservative 2; Mismatches 7; Indels
                                                                              EMBL; Z28084; CAA81922.1; -.
PIR; S37909; S37909.
Germonline; 138099; S37909.
GER S0001567; YKL084W.
InterPro; IPR008913; ZF-CHY.
Hypothetical protein:
SEQUENCE 116 AA; 13641 MW; 57464E5FD9A591F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=82103990; PubMed=6172714;
Eiferman F.A., Young P.R., Scott R.W., Tilghman S.M.;
"Intragenic amplification and divergence in the mouse alpha-feoprotein gene.";
Nature 294:713-718(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          605 AA
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SRCVHWHLPKDVIAIRFKC 33
                                                                                                                                                                                                                                                                                                                                                              7 SRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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Nortons P., Narchionni L., Machinan J., Sakamico N., Sasakii H., Safor K., Schombanh C., Saya T., Sinkan V., Scroff K., P., Suzukii H., Safor K., Schombanh C., Saya T., Sinkan V., Scroff K., P., Suzukii H., Safor K., Schombanh C., Saya T., Sinkan V., Scroff K., P., Margarian J., Machinan J., Margarian J., Machinan J., Margarian J
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Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-22494512; PubMed=12606285; Brodigan T.M., Liu J., Park M., Kipreos E.T., Krause M.; Brodigan T.M., Liu J., Park M., Kipreos E.T., Krause M.; Cyclin E expression during development in Caenorhabditis elegans."; Dev. Biol. 254:102-115(2003).
-i- FUNCTION: Essential for the control of the cell cycle at the G1/8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (start) transition.
-!- SUBDATT: Interacts with a member of the CDK2/CDK protein kinases to form a serine/threonine kinase holoensyme complex. The cyclin subunit imparts substrate specificity to the complex (By
                                                                                                                                                                                                                                                                Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          similarity).
-!- SUBCELLULAR LOCATION: Nuclear (By similarity).
-!- SIMILARITY: Belongs to the cyclin family.
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11 cycle, Cell division; Nuclear protein.
518 AA; 59469 MW; A084943B8E8891D3 CRC64;
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Archaea, Buryarchaeota, Halobacteria, Halobacteriales;
Halobacteriaceae, Haloferax.
NCBI_TaxID=2252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GVPC HALME STANDARD; PRT; 381 AA. 002228; 01-UUL-1993 (Rel. 26, Created) 01-UUL-1993 (Rel. 26, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Gas vesicle protein C.
                                                                                               10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
G1/5-specific cyclin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35.5%; Score 50; DB 1
50.0%; Pred. No. 8.3;
tive 2; Mismatches
                                                                                                                                                                                                                                     Caenorhabditis briggsae.
Bukaryota, Metazoa, Nematoda, Chromadores
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00134; cyclin; 1. SMART; SM00385; CYCLIN; 1
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hes 9; Conservative
                                               STANDARD;
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                                               CAEBR
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GVPC_HALME
                       CG1E (
                                               UNTERPRETATION OF STREET AND STRE
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MEDLINE=8305684); PubMed=7142161;
Gingeras T.R., Sciaky D., Gelinas R.E., Bing-Dong J., Yen C.E.,
Kelly M.M., Bullock F.A., Parsons B.L., O'Neill K.E., Roberts R.J.;
"Nucleotide sequences from the adenovirus-2 genome.";
J. Biol. Chem. 257:13475-13491(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-83056844; PubMed=7142162;
Alestroem P., Akusjaervi G., Pettersson M., Pettersson U.;
Alestroem P., Akusjaervi G., Pettersson M., Pettersson U.;
"DNA sequence analysis of the region encoding the terminal protein and the hypothetical N-gene product of adenovirus type 2.";
J. Biol. Chem. 257:13492-13498(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human adenovirus type 2.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36.2%; Score 51; DB 1; Length 106; 62.5%; Pred. No. 1.1; ive 1; Mismatches 5; Indels
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106 AA; 11668 MW; 12692EF62B02E3A3 CRC64;
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CE09E9F50D74619A CRC64;
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PIR; D92351; A03859.
Hypothetical protein Early protein
SEQUENCE 106 AA; 11668 MW; 1269
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10; Conservative
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605 AA;
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Y116 ADE02
ID Y116 ADE02
AC P03287;
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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C P24574; QHI17;
T 01-MAR-1992 (Rel. 21, Created)
T 01-MAR-1992 (Rel. 21, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
N (GVPC1 OR GVPC OR VNG6031G) AND (GVPC2 OR VNG6031G).
N (GVPC1 OR GVPC OR VNG6032G) AND (GVPC2 OR VNG6031G).
S Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081), and S Halobacterium sp. (strain NRC-817).
C Plasmid pNRC100, Plasmid pNRC200, and Plasmid pHH1.
C Archaea; Euryarchaeoca; Halobacteria; Halobacteriales;
C Halobacteriaceae; Halobacterium.
N NCBI TaxID=64091, 148370;
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MEDLINE=91323716; PubMed=1864501;
Jones J.G., Young D.C., Dassarma S.;
"Structure and organization of the gas vesicle gene cluster on "
Halobacterium halobium plasmid pNRC100.";
                                                                                                                                                                                          vesicle membrane.
-!- SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 49.5; DB 1; Length 381; Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X APPROXIMATE TANDEM REPEATS
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9FB48199D0305921 CRC64;
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PIR; S28115; S28115; S28115; InterPro; IPR008639; Halo_GVPC.
Pfam; PF05465; Halo_GVPC; 1.
Gas vesicle; Repeat.
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STRAIN=NRC-1; PLASMID=pNRC100;
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hes 9; Conservative
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                                                                                                                                                                                                                           CYANOBACTERIA.
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SEQUENCE
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GVC1_HALN1
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STRAIN=NRC-817, PLASMID=PHH1;
STRAIN=NRC-817, PLASMID=PHH1;
STRAIN=NRC-817, PLASMID=PHH1;
BRDILINE=93021102; PubMed=1404376;
Englert C., Krueger K., Offener S., Pfeifer F.;
"Three different but related gene clusters encoding gas vesicles in halophilic archaea.",
halophilic archaea.",
N. MOL. 8101. 227:586-592(1992).
-!- FUNCTION: May confer stability to the gas vesicle membranes. Gas vesicles are small, hollow, gas filled protein structures that are found in several microbial planktonic microorganisms. They allow the postitioning of the organism at the favorable depth for growth.
-!- SUBCELLULAR LOCATION: Binds to the external surface of the gas
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-2050483; PubMed=12016950;
MEDLINE-20504483; PubMed=12016950;
MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Shrogna J.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Leithauser B., Kaller K., Pohls T.A., Welti R., Goo Y.A.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Bhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
"Genome sequence of Halobacterium species NRC-1.",
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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MEDLINE=92065812; PubMed=1956294;
Horne M., Englert C., Wimmer C., Pfeifer F.;
"A DNA region of 9 kbp contains all genes necessary for gas vesicle synthesis in halophilic archaebacteria.";
Mol. Microbiol. 5:1159-1174(1991).
        Faust
Ng W.V., Ciufo S.A., Smith T.M., Bumgarner R.E., Baskin D., Faue Hall B., Loretz C., Seto J., Slagel J., Hood L., DasSarma S.; Sapphoto of a large dynamic replicon in a halophilic archaeon: megaplasmid or minichromosome?"; Genome Res. 8:1131-1141(1998).
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SIMILARITY: VERY DISTANT, TO GAS VESICLE PROTEINS TYPE C OF
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4 7 X APPROXIMATE TANDEM REPEATS.
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171DBEB4C0364F46 CRC64;
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EMBL; AE005142; AAG2027.1; -.
EMBL; X5716; CAA4651.1; -.
EMBL; X64729; CAA45881.1; -.
PIR; T08243; T08243.
InterPro; IPR008639; Halo_GVPC.
Pfam; PF03465; Halo GVPC; 1.
Gas vesicle; Plasmid; Repeat; Com
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EMBL; AF016485; AAC82810.1; -.
EMBL; AE005142; AAG20727.1; -.
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169
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254
382 AA;
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SEQUENCE
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Galibert F.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90080148; PubMed=2152825;
Mergia A., Shaw K.E.S., Lackner J.E., Luciw P.A.;
"Relationship of the env genes and the endonuclease domain of the polgenes of simian foamy virus type 1 and human foamy virus.";
J. Virol. 64:406-410(1990).
-!- CAȚALYȚIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  + {DNA}(N).
- PTM: Specific enzymatic cleavages in vivo yield mature proteins.
- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY A9.
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R INTERPROJECT DENOUGES RNASH.

R INTERPROJES NASH.

R PÉRM, PROOUTS; RNASH; 1.

R PÉRM, PROOUTS; RVC; 1.

R PÉRM, PROOUTS; RVC; 1.

R PÉRM, PROOUTS; RNA-directed DNA polymerase; Hydrolase; Nuclease;

M Transferase; RNA-directed DNA polymerase; Hydrolase; Nuclease;

M TRAINTS; PROOUTS; PR
                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-91276270; PubMed-1647358;
Kuptec J.-J., Kay A., Hayat M., Ravier R., Peries J., Galiber'
Kuptec J.-J., Kay B., Hayat M., Ravier R., Peries J., Galiber'
Sequence analysis of the simian foamy virus type I genome.";
Gene 101:185-194(1991).
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                                                                 01-NOV-1991 (Rel. 20, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
01-UUL-1993 (Rel. 41, Last annoctation update)
POL polyprotein [Contains: Protease (BC 3.4.23.-); Reverse transcriptase (BC 2.7.7.49); Endonuclease].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-970 FROM N.A.
MEDLINE-91361538; PubMed=1653483;
Mergia A., Luciw P.A.,
"Replication and regulation of primate foamy viruses.";
Virology 184:475-482(1991).
                                                                                                                                                                                                                      POL.
Simian foamy virus (type 1) (SFV-1).
Viruses; Retroid viruses; Retroviridae; Spumavirus.
NCBI_TaxID=11964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 48; DB
Pred. No. 38;
5; Mismatches
                          1161 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X54482; -; NOT ANNOTATED_CDS.
EMBL; X58484; CAA41394.1; -.
EMBL; M335G1; AAA47793.1; -.
PIR; A335G2; A335G2.
PIR; S155G6; S155G6.
HSSP; PO3355; IMML.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 969-1161 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.08;
47.48;
                          STANDARD;
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Best Local Similarity
Matches 9; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEROPS; A09.001;
                       POL_SFV1
P23074;
                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnollophyta, eudicotyledons, core eudicots; rosids; eurosids I, Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. Alaska; TISSUE=Apical bud; MEDLINE=99406511; PubMed=10476071; MEDLINE=99406511; PubMed=10476071; Marsh J.F. III, Kaufman L.S.; (Cloning and characterisation of PGA1 and PGA2: two G protein alpha-subunits from pea that promote growth in the yeast Saccharowyees cerevisiae."; Plant J. 19:237-247(1999).
-!- FUNCTION: Guanine nucleotide-binding proteins (G proteins) are involved as modulators or transducers in various transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           signaling systems.
SUBUNIT: G proteins are composed of 3 units; alpha, beta and
gamma. The alpha chain contains the guanine nucleotide binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: Belongs to the G-alpha family. Subfamily 2 (G(s)).
                                                                                                                                                                                                                                                                                                                                                                  15-DEC-1998 (Rel. 37, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Guanine nucleotide-binding protein alpha-2 subunit (GP-alpha-2)
GPA2 OR GA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

GDP-RIBOSYL[1] (BY ACTION OF CTX).

GB0963393PD20BA4 CRC64;
Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.0%; Score 48; DB 1; Length 384; 50.0%; Pred. No. 12; 4; Indels ive 4; Mismatches 4; Indels
                                                        Indels
Score 49.5; DB 1;
Pred. No. 7.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; T06814; T06814.
HSP: PLO824; LAS3.
INTERPRO; IPR001019; Gprotein_alpha.
PEam; PP00503; G-alpha; 1.
PRINTS; PR0018; GPROTEIN.
ProDom; PD000281; Gprotein_alpha; 1.
SMART; SM00275; G-alpha; 1.
GTP-binding; Transducer; ADP-ribosylation.
NP_BIND
46 53
                                                                                                                                                                                                                                                                                                               384 AA
7 Match 35.1%; Score 49.5; D
Local Similarity 64.3%; Pred. No. 7.1;
tes 9; Conservative 1; Mismatches
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SRLDYPHLTKDLAKEI 140
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                                                                                                                                                    344 CGE-YYQAITEPHL 356
                                                                                                                 1 CGETYYSRVTHPHL 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pisum sativum (Garden pea)
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                                                                                                                                                                                                                                                                                                               STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3888;
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004279;
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        Query Match
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215 EVWGSSVMHPWLPKEQOSSILK 236
STY0816 OR T2104.
                                                                                                                                                      SEQUENCE FROM N.A.
MODC OR STY0816 (
Salmonella typhi
                                                                                                    NCBI_TaxID=601;
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NEDLINE-2282867; PubMed=12949112;

Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,

Bisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.,

Baten J.A., Paugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.,

A Haft D.H., Kolonay J.F., Nelson W.C., Mason T., Tallon L., Gray J.,

A Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,

A Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,

A Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,

A Dewhirst F.E., Fraser C.M.;

Toophyromons agnalyable strain W83.";

J. Bacteriol. 185.5591-560[2003)

C -- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) = AMP +

Alphosphate + L-tryptophanyl-tRNA (Trp)

C -- SUBGINIT: Homodimer (By similarity)

C -- SUBGINIT: Belongs to class-I aminoacyl-tRNA synthetase family.

C -- SUBCELIULAR LOCATION: Cytoplasmic.

C -- SUBICART Belongs to class-I aminoacyl-tRNA synthetase family.

C -- SUBICART Belongs to class-I aminoacyl-tRNA synthetase family.

C -- SUBICART Belongs to class-I aminoacyl-tRNA synthetase family.

C -- SUBICART Belongs to class-I aminoacyl-tRNA synthetase family.

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PROSITE; PS00178; AA TRNA LIGASE I; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                            15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
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                                                                                                                                                                                                                                                                                                                                                                                               Porphyromonas gingivalis (Bacteroides gingivalis).
Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
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10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Molybdenum import ATP-binding protein modC (EC 3.6.3.29).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "MMSKS" REGION.
ATP (BY SIMILARITY).
C3BBA8983DC34FCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 352 AA
                                                                                                                                                                                    327 A.A.
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                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 18 "HL
194 198 "KN
197 197 ATE
327 AA; 36969 MW; C
                                    |: |:| ||:| ||:| || 840 SKYWWPNLRKDVVKSIRQC 858
        7 SRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 WHSLTTHPH-PDNIVRNV 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE017179; AAQ67045.1; -.
                                                                                                                                                                                                                                            15-MAR-2004 (Rel. 43, Created)
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                                                                                                                                                                                          STANDARD;
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Best Local Similarity
9; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           (S).
OR PG2085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=837;
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Q8Z8A4;
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BINDING
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-!- FUNCTION: Part of the ABC transporter complex modABC (TC 3.A.1.8)
involved in molybdenum import. Responsible for energy coupling to
the transport system (By similarity).
-!- CATALYTIC ACTIVITY: ATP + H(2)O + molybdate(Out) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  + molybdate(In).
-!- SUBUNIT: The complex is composed of two ATP-binding proteins (modd), two transmembrane proteins (modB) and a solute-binding protein (modA) (Probable).
-!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
-!- SUBCELLULAR LOCATION: Inner membrane-associated (By similarity).
                                                                                                                                                                                                                     MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungall K.L., Benelley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingwicht T., Connerton P.,
Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J.,
Cronin A., Larsen T.S., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella
enterica serovar Typhi CT18";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRANT-172 / Arcc 700931;
STRANT-172 / Arcc 700931;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoylanni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2 and CT18";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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TIGREAMS; TIGROUGSS MOD; 1.

PROSITE; PS00211; ABC_TRANSPORTER_1; 1.

PROSITE; PS50831; ABC_TRANSPORTER_2; 1.

Hydrolase; Transport; Molybdenum; Membrane; Inner membrane; ATP-binding; Complete proteome.
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Interpro; IPR003493; ABC_transporter.
Interpro; IPR004606; MOP_Interpro; IPR008995; MOP_like.
Interpro; IPR008106; TOBE.
Pfam; PF004005; ABC_tran; 1.
Pfam; PF03459; TOPE; 1.
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RESULT 15
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                                                                                                                                                                                                                                                   DEACLE FROM W. M. STREATHS / ATCC 700720;

WEDLINE=21534948; PubMed=11677609;

MEDLINE=21534948; PubMed=11677609;

MCTClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J. Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K., "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                            Nature 413:852-856 (2001).
-!- FUNCTION: Part of the ABC transporter complex modABC (TC 3.A.1.8) involved in molybdenum import. Responsible for energy coupling to the transport system (By similarity).
-!- CATALYTIC ACTIVITY: ATP + H(2)O + molybdate(Out) = ADP + phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Inner membrane-associated (By similarity). SIMILARITY: Belongs to the ABC transporter family. ModC subfamily.

    + molybdate(In).
    -!- SUBUNT: The complex is composed of two ATP-binding proteins (modC), two transmembrane proteins (modB) and a solute-binding protein (modA) (Probable).

                                                                                                                                                                   Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00211; ABC TRANSPORTER 1; 1.
PROSITE; PS50893; ABC TRANSPORTER 2; 1.
Hydrolase; Transport; Molybdenum; Membrane; Inner membrane;
ATP-binding; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; Score 47; DB 1; Length 352; 50.0%; Pred. No. 15; tive 2; Mismatches 9; Indels
                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last semnotation update)
Molybdenum import ATP-binding protein modC (EC 3.6.3.29)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NP BIND 31 38 ATP (By similarity). SEQUENCE 352 AA; 39055 MW; 65137E645711AAB5 CRC64;
                                                            352 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003593, AAA ATPase.
InterPro; IPR003439; ABC_transporter.
InterPro; IPR004606; Mop.
InterPro; IPR00895; Mop like.
InterPro; IPR00895; MoP like.
InterPro; IPR005116; TOBE.
Pfam; PP00405; ABC tran; 1.
SMART; SM00382; AAA; 1.
TIGRFAMS; TIGR0638; Mop; 1.
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nes 11; Conservative
                                                            STANDARD;
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                       MODC OR STM0783
                                                                                                                                                                                                               NCBI_TaxID=602;
                                                           MODC_SALTY
Q8ZQR6;
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Gaps

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
lamiids; Solanales; Solanaceae; Solanum.
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-!- SUBUNIT: G proteins are composed of 3 units; alpha, beta and
gamma. The alpha chain contains the guanine nucleotide binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein alpha subunit.";
Gene 107.189-195 (1991).
-!- FUNCTION: Guanine mucleotide-binding proteins (G proteins) are
involved as modulators or transducers in various transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: Belongs to the G-alpha family. Subfamily 2 (G(s)).
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=cv. VF36; IISSUE=Pistil;
MEDLINE=92084110; PubMed=1748292;
MM H., Yanofsky M.F., Huvan H., Yanofsky M.F., Hanolation and sequence analysis of TGA1 cDNAs encoding a tomato
                                                 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-MAR-2004 (Rel. 43, Last amnotation update)
Guanine nucleotide-binding protein alpha-1 subunit (GP-alpha-1).
GPAAL OR GAI.
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GTP (BY SIMILARITY).

GTP (BY SIMILARITY).

ADP-RIBOSYL [1] (BY ACTION OF CTX)

5 COSED74EFC01AOA CRC64;
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PIR, JH0514; RGT00A.
HSSP; P10824; 1AS3.
INTEXPRO; IPRO01019; Gprotein_alpha.
Pfam; PR00503; G-alpha; 1.
PRINTS; PR00318; GPROTEINA.
ProDom; PD000281; Gprotein_alpha; 1.
SWART; SM00275; G_alpha; 1.
GTP-binding; Transducer; ADP-ribosylation.
NP_BIND
A6 53 GTP (BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Search completed: February 26, 2004, 08:24:20 Job time : 8.4 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4081;
GBA1_LYCES
ID GBA1_LYCES
AC P26981;
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us-09-701-623c-6.rspt

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ID Q8SD16
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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sp_virus:*
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Perfect score:
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0312x0 arabidopsis
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03444 homo sapien
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043199 pisum sativ
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08139 streptomyce
08xy27 streptomyce
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Q7ULT4
Q8U0E1
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Q91Z67
Q90544
Q94FR5
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087052
08JRY8
097IP8
08LJQ9
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Q8W3P1
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Q8W3P4
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Q893F1
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ALIGNMENTS

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Gaps
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MEDLINE=21914557; PubMed=11916376;
Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
Mostyanzhinov V.V., Sybben J., Grymonprez B., Kostyuchenko V.A.,
Bourkaltseva M.V., Sykilinda N.N., Krylov V.N., Volckaert G.,
"The genome of bacteriophage phiKZ of Pseudomonas aeruginosa.";
J. Mol. Biol. 317:1-19(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                    [2] SEQUENCE FROM N.A. Mebben J., Grymonprez B., Kostyuchenko V.A., Meyanzhinov V.V., Sykilinda N.N., Krylov V.V., Volckaert G.; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF599011; AA483047.1; -
Interpro; IFPR098160; Collagen.
Pfam; PF01391; Collagen; 2. SEOUENCE 1093 AA; 115835 MW; D755B6C65D910DF7 CRC64;
                                                                                                                                                   Pseudomonas phage phiKZ.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
NCBI_TaxID=169683;
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Best Local Similarity 39.1%; Pred. No. 6.6;
Matches 9; Conservative 7; Mismatches 7; Indels
                                                  Created)
Last sequence update)
Last annotation update)
PRT; 1093 AA.
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                                         (TrEMBLrel. 21, C (TrEMBLrel. 21, I (TrEMBLrel. 24, I
  PRELIMINARY;
                             Q8SD16;
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
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us-09-701-623c-6.rspt

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SEQUENCE FROM N.A.
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SEQUENCE
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X MEDILINE=21287275; PubMed=11381131;

AEDILINE=21287275; PubMed=11381131;

A Zagmitko O., Jelenska J., Tevzadac G., Haselkorn R., Gornicki P.;

Tan isoleucine/leucine residue in the carboxyltransferase domain of acetyl-CoA carboxylase is critical for interaction with acetyl-CoA carboxypropionate and cyclohexanedione inhibitors.";

Taryloxyphenoxypropionate and cyclohexanedione inhibitors.";

Proc. Natl. Acad. Sci. U.S.A. 98:6617-6622(2001).

R BMBL; AR359518; AAK62314.1; -...

GO; GO:00004075; F:biottin carboxylase complex; IEA.

R GO; GO:0004075; F:biottin carboxylase activity; IEA.

InterPro; IPR000022; Carboxyl_trans.

Pfam; PF01039; Carboxyl_trans; 1.

T NON_TER 1078 1078

SEQUENCE 1078 AA; 120645 MW; OACFCBBEBD794CD1 CRC64;
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                                                                                               Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
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Spermatophyta; Magnoliophyta; Liliopaida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                                                                                                         "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 288:2012-2018(1998). EMBL; Z92827; CAB07326.1; -. PIR; T19571; T19571.
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                                                                                                                                                                    McMurray A.A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                WormPep; C29F7.1; CE08442.
InterPro; IPR04119; DUF227.
Pfam; PF02958; DUF227. 1.
SMART; SM00587; CHK; 1.
SEQUENCE 394 Aa; 44297 MW; D4424A972AE24451 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Acetyl-CoA carboxylase (Fragment)
                                     Last sequence update)
Last annotation update)
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394 AA
                          Created)
PRT;
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                      01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2003 (TrEMBLrel. 24,
C29F7.1 protein.
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Best Local Similarity 55.6
Matches 10; Conservative
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PRELIMINARY;
                                                                                        Caenorhabditis elegans.
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Beet Local Similarity
9; Conserva
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Plant Mol. Biol. 24:35-49(1994).
-!- FUNCTION: THIS PROTEIN CARRIES THREE CATALYTIC FUNCTIONS: BIOTIN CARBOXYLASE, AND CARBOXYLTRANSFERASE.
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MEDINE-2. DK592.

MEDINE-2.1287275; PubMed=11381131;

MEDINE-2.297275; PubMed=11381131;

An isoleuchne/leucine residue in the carboxyltransferase domain of acetyl-CoA carboxylase is critical for interaction with arryloxyphenoxypropionate and cyclohexanedione inhibitors.";

Proc. Natl. Acad Sci. U.S.A. 98:6617-6622(2001).

BMB1. ARS2917; ARK2213.1;

GO; GO:0009343; C:biotin carboxylase activity; IEA.

GO; GO:000943; C:biotin carboxylase activity; IEA.

InterPro; IPR000022; Carboxyl_trans.

Pfam; PF01039; Carboxyl_trans.

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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
PACCAD clade, Panicoideae, Andropogoneae, Zea.
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MEDINE=9415421; PubMed-7906562;
Ashton A.R., Jenkins C.L., Whitfeld P.R.;
"Molecular cloning of two different cDNAs for maize acetyl CoA
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01-NOV-1996 (TERMBLrel. 01, Created)
01-NOV-1996 (TERMBLrel. 01, Last sequence update)
01-OCT-2003 (TERMBLrel. 25, Last annotation update)
01-OCT-2003 (TERMBLRel. 25,
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                                                                                                                                                                                                                                                                                                                Q94FR7 PRELIMINARY; PRT; 1079 AA. Q94FR7; 101DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                         350 ETYISRLYQPHLVKDSIQ 367
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RIYYSRVTHPHLPKDIVR 20
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Matches 10; Conservative
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NCBI_TaxID=4577;
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Q41743;
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Matches
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MEDLINE-98054381; PubMed-9391173;

Gornicki P., Faris J., Podkowinski J., Gill B., Haselkorn R.;

Gornicki P., Faris J., Podkowinski J., Gill B., Haselkorn R.;

Gornicki P., Faris J., Podkowinski J., Gill B., Haselkorn R.;

Franciscus J., Faris J., Podkowinski J., Jead wheat is encoded by a single gene on each of the three ancestral chromosome sets.";

Proc. Natl. Acad. Sci. U.S.A. 94:14179-14184(1997).

EMBL; AF029895; AAC39331.1; -.

PIRSP; 706161; 706161.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
-1- COFACTOR: BIOTIN.
-1- ENZYME REGULATION: BY PHOSPHORYLATION.
-1- PATHWAY: FIRST STEP (RATE LIMITING) IN LONG-CHAIN FATTY ACID
                                                                                                                                                                                                                                                                                                                    This is 10221; Indiana carboxylase complex; IEA.

GO; GO:0003943; C:biotin carboxylase activity; IEA.

GO; GO:000394; F:biotin binding; IEA.

GO; GO:00094075; F:biotin carboxylase activity; IEA.

GO; GO:0016874; F:ligase activity; IEA.

GO; GO:0006833; P:fatty acid biosynthesis; IEA.

InterPro; IPR000022; Carboxyl Lrans.

Pfam; PP001039; Carboxyl trans.

Pfam; PP01039; Carboxyl trans.

Pfam; PP01039; Carboxyl trans.

Pfam; PP01039; Carboxyl trans.

Pfam; PP01039; Carboxyl trans.

Pfatty acid biosynthesis; Biotin; Ligase; Multifunctional enzyme.
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                                                                                                                       -i-SIBUNIT: HOMOTETRAMER.
-i-SUBUNIT: HOMOTETRAMER.
-i-SIMILARITY: PARTIAL TO CARBAMYL PHOSPHATE SYNTHETASES.
EMIL, 22449; CAA80822.1; -
PIR; S42659; S42659.
PIR; T02221; T02221.
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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CO.0009343; C:biotin carboxylase complex; IEA.
GO:0005524; F:ATP binding; IEA.
GO:0004075; F:biotin carboxylase activity; IEA.
GO:0016844; F:ligase activity; IEA.
GO:0008152; P:metabolism; IEA.
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GO; GO:0004075; F:Biotan carboxylase a
GO; GO:0004075; F:Biotan carboxylase a
GO; GO:0004152; P:Bidsan carboxylase
GO; GO:0004152; P:Bidsan carboxylase
InterPro; IPR000840; Bidtin lipoyl.
InterPro; IPR000089; Bidtin lipoyl.
InterPro; IPR000409; Carboxyl trans.
InterPro; IPR005419; Carboxyl trans.
InterPro; IPR005419; Carboxyl trans.
Pfam; PF02785; Bidtin carb_C; I.
Pfam; PF03089; Carboxyl trans.
IPFam; PF00389; Carboxyl trans.
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les 10; Conservative
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                                                                                                     SYNTHESIS.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
fill TaxID=4577;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                      38.3%; Score 54; DB 10; Length 2311; 55.6%; Pred. No. 43; ive 3; Mismatches 5; Indels
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY312171; AAP78896.1; -.
SEQUENCE 2324 AA; 257167 WW; 4E2249B04E7066A6 CRC64;
Pfam; PF02786; CPSase L D2; 1.
PROSITE; PS00867; CPSASE 2; 1.
SEQUENCE 2311 AA; 254970 MW; IBBC5CDD0F9F984B CRC64;
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SEQUENCE FROM N.A.
STRAINS-A188; TISSUE=Leaf;
MEDLINE=37420; PubMed=7630949;
Bgli M.A., Lutz S.M., Somers D.A., Gengenbach B.G.;
Bmbli M.A., Tocensy, 1300 (1995).
BMBL, U19183; AAA80214.1;
BIR; SAZ659; SAZ659.
BIR; TOZ235; TOZ235.
HSSP; P24182; LDVI.
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01-OCT-2003 (TYEMBLrel. 25, Last sequence update)
01-OCT-2003 (TYEMBLrel. 25, Last annotation update)
Acetyl.coenzyme A carboxylase ACCIA.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Acetyl-coenzyme A carboxylase.
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                                                                                                                                       ilarity 55.6%;
Conservative
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Best Local Similarity
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ses 10; Conserv
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us-09-701-623c-6.rspt

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STRAIN=CV. Columbia;
MEDLINEA20083487; Pubmed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fuji C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Bueil C.R., Ketchum K.A., Lee J.T., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M. Vanken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.,
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
"Macropodid herpesvirus 1 and 2: unique short region glycoproteins."; Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

BMBL, AYO48539; AAL13140.1; -...
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR003104; Herpes_glycopE.
InterPro; IPR00710; Ig-11ke.
PEam; PF02480; Herpes_gE; EA.
SEQUENCE 532 AA; 59087 WW; 567D44D52600B76B CRC64;
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Spermatophyta, Magnoliophyta; eudicocyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae, Arabidopsis.
NCBI_TaxID=3702;
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Pred. No. 66;
6; Mismatches 9; Indels C
                                                                                                                                                                                                                                            37.6%; Score 53; DB 12; Length 532; 44.4%; Pred. No. 13;
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EMBL; AC004705; AAC24188.1; -.
ENBL; AC004705; AAC24188.1; -.
GO; GO:0008213; F: cysteine-type peptidase activity; IEA.
GO; GO:0006508; P: proteolysis and peptidolysis; IEA.
InterPro; IPR003653; Peptidase C48.
Pfam; PF02902; Peptidase C48.
PROSITE; PSS0600; ULP PROTEASE; 1.
SEQUENCE 1756 AA; I97368 MW; 68FC3BSFCC282775 CRC64;
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Last annotation update)
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AT2G14770.
Arabidopsis thaliana (Mouse-ear cress).
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Local Similarity 37.5%;
es 9; Conservative
                                                                                                                                                                                                                                                                           ilarity 44.4%;
Conservative
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Nature 402:761-768(1999)
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STRAIN=cv. Columbia;
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12, Conserv
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QBBK65;
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QBBK65
ID QBBK6
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Wkaryots, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
PACCAD clade, Panicoldeae, Andropogoneae, Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. TISSUE=Callus; STAIN=Cv. Zong31; TISSUE=Callus; Zhao H., Wang G.; "Cloning of chloroplast acetyl-CoA carboxylase cDNA from Zea mays
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        R GO; GO:0016874; F:ligase activity; IEA.
R GO; GO:0016874; F:ligase activity; IEA.
GO; GO:00018152; P:metabolism; IEA.
R InterPro; IPR001682; Biotin_lipoyl.
R InterPro; IPR001689; Biotin_lipoyl.
R InterPro; IPR005479; CPase_L_D2.
R InterPro; IPR005479; CPase_L_D2.
R InterPro; IPR005481; CPase_L_D.
R Pfam; PR01038; Biotin_lipoyl; 1.
R Pfam; PR01039; CPase_L_D4: 1.
R Pfam; PR01039; CPase_L_D4: 1.
R Pfam; PR01039; CPase_L_D4: 1.
R Pfam; PR01089; CPase_L_D4: 1.
R Pfam; PR01088; CPase_L_D4: 1.
R PR0SITE; PS01087; CPSASE_Z; 1.
S EQUENCE 2325 AA; 257150 MW; ECBOAEF3FE26FE0C CRC64;
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Macropodid herpesvirus 1.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Simplexvirus.
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Last annotation update)
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Best Local Similarity 55.6%;
Matches 10; Conservative
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Thomson D., Smith G.;
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NCBI_TaxID=29292;
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the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the Nature 420:563-573 (2002).
The Nature 420:673 (2002).
The Nature 420:673 (2002).
The Nature 1 reproduction; IMP.
The Nature 1 PRO00264; Serum albumin.
The Nature 1 PRO00264; Serum albumin.
The Nature 1 PRO00213; transport Proct; 3.
The Nature 1 PRO00214 (2002).
The Nature 1 PRO00214 (2002
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STRAIN-GS-SHL/GG 17 INSUE-Placenta, and Extraembryonic tissue;
MEDINE-GS-14683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
MAILYS 420:655-573 (2002).
EMBL; AK076197; BAG36249-1; -.
MOD; MG1:87951; AFP.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus.
NCBI_TaxID=10090;
                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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PROSITE; PS00212; ALBUMIN; 2.
SEQUENCE 605 AA; 67322 MW; 048B7A4A8B01EA4B CRC64;
01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Alpha-fetoprotein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=22354683; PubMed=12466851;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                          The FANTOM Consortium,
                                                                                                                                        (Mouse)
                                                                                                                                                                                                                                                                           SECUENCE FROM N.A.
                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                   musculus
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Submitted (JDL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248284; CAB49448.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                      DB 11; Length 605;
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                                                                                                       Indels
SMART; SM00103; ALBUMIN; 3.
PROSITE; PS00212; ALBUMIN; 2.
SEQUENCE 605 AA; 67409 MW; CF3509A9EC146110 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein PYRAB05260.
PYRAB05260 OR PAB0359.
                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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                                                                  36.5%; Score 51.5; Ilarity 57.9%; Pred. No. 25; Conservative 3; Mismatches
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44.4%; Pred. No. 30;
tive 1; Mismatches
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                                                                                                                                           6 YSRVTHPHLPKDIVRSIAK 24
                                                                                                                                                                                                                                                                                                     01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
05UNBA0014F04.20, protein.
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Conservative
                                                                                                                                                                                                                                                                     PRELIMINARY;
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STRAIN-GE5 / Orsay;
Heilig R.;
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ses 16; Conserva
                                                                                     Local Similarity
hes 11; Conserv
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HSSP; Q58292; 1DUS.

QC) GO:0008737; F:S-adenosylmethionine-dependent methyltransf. . .; IEA.
InterPro; IPR000081; SAM_bind.
InterPro; IPR000081; SAM_bind.
Fram; PF05175; MTS; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 195 AA; 21778 MW; 471178A62097C02C CRC64;
                                                                                                                                                                        2; Gaps
                                                                                                                                     Query Match 36.2%; Score 51; DB 17; Length 195; Best Local Similarity 47.8%; Pred. No. 8.9; Matches 11; Conservative 5; Mismatches 5; Indels
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Search completed: February 26, 2004, 08:27:14 Job time : 35.4 secs

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Sequence 3, Application US/10152190
Publication No. US20030096369A1
GENERAL INFORMATION:
APPLICANT: MORANDA MANAMADA A.
TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgE vaccines
FILE REFERENCE: PC11011A
CURRENT APPLICATION NUMBER: US/10/152,190
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 2
US-10-152-190-3
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Sequence 3, Appli
Sequence 2, Appli
Sequence 11, Appl
Sequence 11, Appli
Sequence 11, Appli
Sequence 12, Appli
                                                                                                                          Pebruary 26, 2004, 08:27:32 ; Search time 26.2 Seconds
    (without alignments)
    201.482 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Published Applications Ah:*

1. /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2. /cgn2_6/ptodata/2/pubpaa/Der_Maw PUB.pep:*

3. /cgn2_6/ptodata/2/pubpaa/Der_Maw PUB.pep:*

4. /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5. /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

6. /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

7. cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

8. /cgn2_6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

9. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

10. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

11. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

12. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

13. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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15. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

16. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

17. /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

18. /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*

19. /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*

17. /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*

18. /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*

18. /cgn2_6/ptodata/2/pubpaa/US00_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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# US-10-152-190-3
# US-10-152-190-3
US-90-401-664-11
US-10-176-664-11
US-10-176-664-11
US-10-152-190-10
US-10-152-190-10
US-10-152-190-11
US-10-152-190-11
US-10-355-161A-10
US-10-355-161A-11
US-10-355-161A-11
US-10-479-614-14
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                                                                                                                                                                                                                                                                                                                                                             809742 seqs, 211153259 residues
                                                                                                                                                                                                                                  141
1 CGETYYSRVTHPHLPXDIVRSIAKC 25
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Maximum Match 100%
Listing first 45 summaries
                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
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Sequence 25, Appl
Sequence 2, Appl
Sequence 10, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 6, Appl
Sequence 1, Appl
Sequence 329, Appl
Sequence 329, Appl
Sequence 1, Appli
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                                                                                                                                                                                                                                                                                                                                                                                   | Sequence 1, Application US/10152190
| Publication No. US20030096369A1
| GENERAL INFORMATION No. US20030096369A1-anaphylactogenic IgE vaccines
| APPLICANT: Morsey, Mohamad A.
| TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgE vaccines
| FILE REFERENCE: PC11011A
| CURRENT APPLICATION NUMBER: US/10/152,190
| CURRENT PILING DATE: 2002-05-21
| NUMBER OF SEQ ID NOS: 28
| SOFTWARE: PatentIn Ver. 2.1
| SEQ ID NO 1
| LENGTH: 114
| TYPE: PRT | APPLICANT OF COMPANIES | CORGANISM: Dog CH3 domain
| US-10-152-190-1
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 Sequence 2, A
Sequence 29,
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0 US-09-479-614-29

0 US-09-479-614-29

4 US-10-214-5-29

103-10-409-772-29

103-10-409-772-29

103-10-409-772-29

103-10-176-664-10

103-10-176-664-10

103-10-176-664-10

103-10-176-10-4

103-10-176-10-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-4

103-10-182-190-8

103-10-182-190-8

103-10-182-190-13
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US-09-949-375A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 GETYYCRVTHPHLPKDIVRSIAK 106
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RESULT 5
US-10-176-664-11
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Sequence 2, Application US/10152190

Sequence 2, Application US/10152190

Publication No. US20030096369A1

GENERAL INFORMATION: No. US20030096369A1-anaphylactogenic IgE vaccines

TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgE vaccines

FILE REFERENCE: PC11011A

CURRENT APPLICATION NUMBER: US/10/152,190

CURRENT PILING DATE: 2002-05-21

NUMBER OF SEQ ID NOS: 28

SOUTWARE: Patentin Ver. 2.1

SEQ ID NO 2
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Best Local Similarity 95.7%; Pred. No. 2.2e-09;
Matches 22; Conservative 0; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , OTHER INFORMATION: Synthetically generated proteins US-09-401-636-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 11, Application US/09401636
Fatent No. USCO1003843A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILLE REFERENCE: 10223/006001
CURRENT PILING DATE: 1999-09-22
FRIOR APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
LENGTH: 341
                                                          TYPE: PRT ORGANISM: Human CH3/dog CH3 domain chimera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Human CH3/dog CH3 domain fusion
                                                                                                                                                                                                                                             85 GETYYCRVTHPHLPKDIVRSIAK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 GETYYCRVTHPHLPKDIVRSIAK 228
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Best Local Similarity 95.79
....nhes 22; Conservative
SOFTWARE: Patentin Ver. 2.1
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US-09-401-636-11
                                    LENGTH: 115
                                                                                               US-10-152-190-3
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                   SEQ ID NO 3
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US-10-152-190-10
Sequence 10, Application US/10152190
Fublication No. US20030096369A1
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgE vaccines
FILE REPRENCE: PC11011A
CURRENT APPLICATION NUMBER: US/10/152,190
CURRENT PILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
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Publication No. US20030096369A1
GENERAL INFORMATION:
APPLICANT: MOTSEY, Mohamad A.
TITLE OF INVENTION: NO. US20030096369A1-anaphylactogenic IgE vaccines
FILE REFERENCE: PC11011A
CURRENT APPLICATION NUMBER: US/10/152,190
CURRENT FILING DATE: 202-05-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: Synthetically generated proteins
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Sequence 11, Application US/10176664
Sequence 11, Application US/10176664
Sequence 11, Application US/10176664
Seneral INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFRENCE: 1022/106001
CURRENT APPLICATION NUMBER: US/09/401,636
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR PILING DATE: 1999-10-22
PRIOR PLILNG DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PASLEEQ for Windows Version 4.0
SEQ ID NO 11
IENGTH: 341
TYPE: PRT
PREMIUM ARTIFICIAL SEQUENCE
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| LENGTH: 346

| TYPE: PRT

| ORGANISM: IGE-1 fusion protein

US-10-152-190-10
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Matches 22; Conserva
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us-09-701-623c-6.rapb

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RESULT 12
US-10-076-674-11
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LENGTH: 44
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; Sequence 28, Application US/10214524
; Publication No. US20030073142A1
; GENERAL INFORMATION:
    APPLICANT: Chen, Swey-Shen Alex
; APPLICANT: Barankiewicz, Theresa J.
    APPLICANT: Barankiewicz, Theresa J.
    APPLICANT: Chen, Zhong
; TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
; FILE REFERENCE: IGE-00101.P.1.1
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/312,120
; PRIOR PELING DATE: 2001-08-13
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 28
; LENGTH: 426
; WODEN: DATE: PATENTIAL PATE
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US-10-152-190-11

US-10-152-190-11

Sequence 11, Application US/10152190

Publication No. US20030096369A1

GENERAL INFORMATION:

APPLICANT: Moreey, Mohamad A.

TITLE OF INVERNION: No. US20030096369A1-anaphylactogenic IgE vaccines

TITLE REPERENCE: PC1101A

TITLE REPERENCE: PC1101A

CURRENT APPLICATION NUMBER: US/10/152,190

CURRENT FILING DATE: 2002-05-21

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PatentIN Ver. 2.1

SEQ ID NO 11

INFOGRAPINA 348

TYPE: PRT

ORGANISM: IGE-2 fusion protein
US-10-152-190-11
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Best Local Similarity 95.7%; Pred. No. 9.1e-09;
Matches 22; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                              Query Match
Best Local Similarity 95.7%; Pred. No. 7.3e-09;
Matches 22; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    213 GETYYCRVTHPHLPKDIVRSIAK 235
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; ORGANISM: Dog (Canis familiaris)
US-10-214-524-28
; SEQ ID NO 12
; LENGTH: 347
; TYPE: PRT
; ORGANISM: IGE-3 fusion protein
US-10-152-190-12
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TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System FILE REFERENCE: Immunogen Delivery System CURRENT APPLICATION NUMBER: US/10/355,161A

CURRENT PILING DATE: 2003-01-31

PRIOR APPLICATION NUMBER: US 10/076674

PRIOR PILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.1

LENGTH: 44
RESULT 10
US-10-076-674-10
INS-10-076-674-10
Sequence 10, Application US/10076674
Sequence 10, Application WS/10076674
GENERAL INFORMATION:
APPLICAT: Sokoll, Kenneth K.
TILLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
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TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
76.6%; Score 108; DB 14;
Best Local Similarity 72.0%; Pred. No. 2.1e-08;
Matches 18; Conservative 3; Mismatches 4;
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US-10-355-161A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature

LOCATION: (19)...(19)

OTHER INFORMATION: Xaa indicates epsilon-Lys

US-10-076-674-10
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; Sequence 10, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
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Best Local Similarity
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ORGANISM: Human
FEATURE:
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ORGANISM: Human
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US-10-355-161A-11
; Sequence 11, Application US/10355161A
; Publication No. US20040009897A1
; GENERAL INFORMATION:
; APPLICANT: SOKOll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT PILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NOS: 13
; SEQ ID NO : 13
; SEQ ID NO : 13
                                                                                                                                                                                                                                                                     Query Match
76.6%; Score 108; DB 14; Length 45;
Best Local Similarity 72.0%; Pred. No. 2.2e-08;
Matches 18; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 76.6%; Score 108; DB 15; Length 45; Best Local Similarity 72.0%; Pred. No. 2.2e-08; Matches 18; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                               . LOCATION: (20) ... (20)
. OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-11
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; OTHER INFORMATION: Xaa indicates epsilon-Lys US-10-355-161A-11
CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SSCTWARE: PatentIn version 3.1
LENGTH: 45
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US-09-479-614-14
'Sequence 14, Application US/08479614
'Sequence 14, Application No. US20030013183A1
'SEGNERAL INFORMATION'S CENERAL INFORMATION'S
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ORGANISM: Human
                                                                                                                                         ORGANISM: Human
                                                                                                                       TYPE: PRT
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TYPE: RT.

(UGRANIEM: PRI)

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Appli Appli

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence

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Query Match 83.7%; Score 118; DB 1; Length 426; Best Local Similarity 95.7%; Pred. No. 5e-11; Matches 22; Conservative 0; Mismatches 1; Indels
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Patent No. 5629415
GENERAL INFORMATION
APPLICANT: HOLLIS, GRECORY F.
APPLICANT: PATEL, MAYUR D.
TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULIN UNWERR OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 126 E. DINCOLN AVENUE
CITY: NEW JERSEY
COUTRY: USB
COUTRY: USB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PREADTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/336,583
FILING DATE: 09-NOV-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: CARTY, CHRISTINE E.
REGISTRATION NUMBER: 19211
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 426 amino acide
TYPE: ATTORNEY/ENESTICS:
TERMADEDNES: Single
US-09-479-614-2

US-08-225-539D-54

US-08-232-539D-56

US-08-644-025A-1

US-08-64-025A-1

US-08-64-025D-18

US-08-232-539D-19

US-08-232-539D-19

US-08-232-539D-19

US-08-232-539D-18

US-08-232-539D-18

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US-08-232-539D-18

US-08-232-539D-18

US-08-232-539D-18

US-08-232-539D-18

US-08-24-151-1

US-08-24-186-9

US-08-695-651-6

US-08-695-6

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126 E. LINCOLN AVENUE
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US-08-336-583-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-336-583-2
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       2. Appli

3. Appli

4. App
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Sequence 95, 7
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1: /cgm2 = / (prodata/2/iaa/5A_COMB.pep:* /cgm2 = / (prodata/2/iaa/5B_COMB.pep:* /cgm2 = / (prodata/2/iaa/6A_COMB.pep:* /cgm2 = / (prodata/2/iaa/6B_COMB.pep:* /cgm2 = / (prodata/2/iaa/PCTUS_COMB.pep:* /cgm2 = / (prodata/2/iaa/Pate/Iles1.pep:* /cgm2 = / (pro
                                           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-100-4148-95
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US-09-100-4148-98
US-09-303-323-99
US-09-303-323-99
US-09-770-014-99
US-09-770-014-99
US-09-770-014-99
US-09-770-014-99
US-09-770-014-99
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US-09-770-014-01
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US-09-303-323-97
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US-09-303-323-102
US-09-770-014-102
US-09-479-614-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389414 seqs, 51625971 residues
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1 CGETYYSRVTHPHLPKDIVRSIAKC 25
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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76.6%; Score 108; DB 3; Length 25;
Best Local Similarity 72.0%; Pred. No. 7.5e-11;
Matches 18; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSES: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCETWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-UNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGETYQSRVTHPHLPRALMRSTTKC 25
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; Sequence 95, Application US/09303323
; Patent No. 6228987
CLASSIFICATION: 424
ATTORNEY/ACENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFRENCE/DOCKET NUMBER: 1151-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-758-4800
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: R. PLOSPY disk
COMPUTER: IBM PC COMPATINE
OPERATING SYSTEM: PC Window
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
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                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-4148-95
                                                                                                                                                                                                                      amino acid
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TOPOLOGY: linear
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TTY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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                                GENERAL INFORMATION:
- APPLICANT: HOLLIS, GREGORY F.
- APPLICANT: HOLLIS, GREGORY F.
- APPLICANT: PATEL, MAYUR D.
- TITLE OF INVENTION: DNA ENCODING CANINE IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSED: CHRISTINE E. CARTY
STREET: 126 E. LINCOLN AVENUE; P.O. BOX 2000
CITT: RAHMAY
CITT: RAHMAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1, Indels
                                                                                                                                                                                                                                                  Query Match 83.7%; Score 118; DB 5
Best Local Similarity 95.7%; Pred. No. 5e-11;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
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ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein PCT-US95-13795-2
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76.6%; Score 108; DB 3;
Best Local Similarity 72.0%; Pred. No. 1.4e-10;
Matches 18; Conservative 3; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-00-100-414B-99
Sequence 99, Application US/09100414B
Fatent No. 6025468
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
DODRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-UNE-1998
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERRINGE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76.6%; Score 108;
                                                                SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATE:
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acids
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TOPOLOGY: linear;
MOLECTLE TYPE: peptide
US-09-100-4148-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-4148-98
     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                        US-09-100-414B-98

Sequence 98, Application US/09100414B

Sequence 98, Application US/09100414B

Patent No. 6025468

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: INWINGENS

TITLE OF INVENTION: INWINGENS

TITLE OF INVENTION: INWINGENS

TORRESPONDENCE ADDRESS:

ADDRESSER: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York

STRATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-UNDE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEC ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 anino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 10154-0054

ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYBE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10154-0054
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                US-09-770-014-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-770-014-95
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Query Match 76.6%; Score 108; DB 3; Length 42; Best Local Similarity 72.0%; Pred. No. 1.4e-10; Matches 18; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Generate No. 6228987
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: INMUNOCENS
INTER OF SOURCES:
ORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STRATE: NA
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER TEADABLE FORM:
MEDIUM TYPE: 10154-0054
COMPUTER: 18 PC COMPATIBLE
OPERATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-198
ATTORNEY/AGENT UNMBER: 29,323
REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 1151-4157
TELERPHONE: 212-758-4800
                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
PRIOR APPLICATION DATE: 10-100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECHONIS: 212-758-4800
TELECHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 CGETYQSRVTHPHLPRALMRSTTKC 42
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Window
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid;
TOPOLOGY: linear;
MOLECTLE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 10
US-09-303-323-99
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                     4; Indels
Best Local Similarity 72.0%; Pred. No. 1.4e-10;
Matches 18; Conservative 3; Mismatches 4
                                                                            RESULT 8
US-09-100-414B-100
; Sequence 100, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; TITLE OF INVENTION: INMUNGENS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTGAN & Pinnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LIRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION UNDER: US/09/100,414B
FILING DATE: 20-UUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEPAX: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                             1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 98, Application US/09303323
Patent No. 6228987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: peptide US-09-100-414B-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 10154-0054
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Sequence 99, Application US/09770014;
Patent No. 655282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: IMMUNOGENS
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: Now York
STATE: NY
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                  FILLING LALLS
CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 09/100,414
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY-AGENT INFORMATION:
NAME: MARIA H. Lin
REGISTRATION NUMBER: 29,323
         NOVEL LHRH PEPTIDE
                                                                                        ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                 COUNTRY: USA

ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
                           IMMUNOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPAX: 212-/2. USORMATION FOR SEQ ID NO. 96 SEQUENCE CHARACTERISTICS: TENGTH: 42 amina acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 72.0
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-770-014-98
      TITLE OF INVENTION: NOT TITLE OF INVENTION: IMMUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
3Y: linear
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US-09-770-014-99
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                                                                                                                                          Length 42;
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                                                                                                                                                                                  4; Indels
                                                                                                                                    Query Match

76.6%; Score 108; DB 3;
Best Local Similarity 72.0%; Pred. No. 1.4e-10;
Matches 18; Conservative 3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                         Sequence 100, Application US/09303323
Fatent No. 6228987
GENERAL INFORMATION:
TITLE OF INVENTION: INMUNOGENS
TITLE OF INVENTION: INMUNOGENS
TITLE OF INVENTION: INMUNOGENS
MUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US 09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION: DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY, AGENT INPORMATION:
NAME: MAATA H. Lin
NAME: MAATA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                     18 CGETYQSRVTHPHLPRALMRSTTKC 42
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                                                                                                                                                                                                                              1 CGETYYSRVTHPHLPKDIVRSIAKC 25
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Patent No. 6559280
GENERAL INFORMATION:
APPLICANT: Mang, Chang Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: mino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-100
                                                                                                                                                                                                                                                                                                                                                           US-09-303-323-100
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US-09-770-014-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE:
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76.6%; Score 108; DB 4; Length 42; 72.0%; Pred. No. 1.4e-10; tive 3; Mismatches 4; Indels
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18 CGETYQSRVTHPHLPRALMRSTTKC 42
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76.6%; Score 108; DB 4; Length 42;
Best Local Similarity 72.0%; Pred. No. 1.4e-10;
Matches 18; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76.6%; Score 108; DB 4; Length 42; 72.0%; Pred. No. 1.4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-770-014-100

Sequence 100, Application US/09770014

Patent No. 6599282

GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LIHRH PEPTIDE
TITLE OF INVENTION: INMUNGENS
NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
FILING DATE: 20-JUNE-1998.
ATTORNEY/AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHAX: 212-758-4800
TELEPAX: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20-UNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: WATIA H. LIN
REGISTRATION WUMBER: 29,323
TELECOMMUNICATION INFORMATION:
TELEFORM: 212-754-8809
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 10154-0054
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: 1: FINGTH: 42 amina acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-100
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 18; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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Query Match 76.6%; Score 108; DB 3; Length 45; Best Local Similarity 72.0%; Pred. No. 1.5e-10; Matches 18; Conservative 3; Mismatches 4; Indels
US-09-100-414B-101

Sequence 101, Application US/09100414B

Sequence 101, Application US/09100414B

Patent No. 602548

GENERAL INFORMATION:
ITILE OF INVENTION: NOVEL LHRH PEPTIDE
ITILE OF INVENTION: NOVEL LHR PEPTIDE
ITILE OF INVENTION: NORTH PEPTIDE
CONFUTER: 145 Park Avenue
STREET: 345 Park Avenue
CITY: New York
STREET: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CLASSIFICATION NUMBER: 29,323
REFERRNCE/POCKET UNDERRY 1157
TELECOMMUNICATION: NUMBER: 29,323
REGISTRATION NUMBER: 29,323
REFERRNCE/POCKET UNDERRY 1151-4157
TELECOMMUNICATION: NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEBRANCE CHARACTERISTICS:
LENGTH + 45 amino acids
TYPE: ATTORNATION acids
TYPE: Amino acids
TYPE: Amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: February 26, 2004, 08:29:26 Job time: 13.6 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 CGETYQSRVTHPHLPRALMRSTTKC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , MOLECULE TYPE: peptide US-09-100-4148-101
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3Y: linear
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GenCore version 5.1.6
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OM protein - protein search, using sw model

February 26, 2004, 08:18:56; Search time 10 Seconds (without alignments) 240.479 Million cell updates/sec Run on:

US-09-701-623C-7 145 1 CGEGYQSRVDHPHFPKPIVRSITKC 25 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	spsilon chain	chain C3 regi	chain C	epsilon chain	epsilon chain	epsilon chain	Ig epsilon-chain -	epsilon ch	class II E	clas	s II his	Lass I	3to	ass	lass I	cell cycle protein	Ig heavy chain pre	ical pr	kinas	kinase C	×	3 RT1.B-b		gamma-1 ch	class I	MHC class II histo	class II h	gamma-1 chain	g gamma-1 chain
	QI	EHRT	I68730	168726	EHWS	S38864	EHWSS	I36948	EHHO	155951	A60497	S10989	HLCHB4	151309	T28149	T28152	AG0531	504845	T23222	T33400	T33399	860117	I54421	S43147	S14236	C60497	3926	B39260	GIMS	GIMSM
	80							N																						
df	Length	429	107	107	388	548	423	426	428	245	264	264	345	355	355	355	430	549	1208	567	597	704	88	110	152	237	266	266	324	393
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	Result No.		7	m	4	2	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

monoclonal antibod hypothetical prote 1g gamma-2a chain hypothetical prote protein T6D22.14 [hypothetical prote hypothetical prote probable cardiolip hypothetical prote desulfoferrodoxin Bolla-DQ beta-1-b	MHC COLI BUTTACE G 32K nonstructural multidrug resistan Ig gamma 3 chain c Ig gamma 1 chain c
PC44436 1499726 17264619 DG6215 BAG2525 B94366 B64366 A4556 A5544	145938 MNIH32 AB3610 I47161 I47158
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### AL IGNMENTS

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RESULT 1
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Igepsilon chain C region - rat

[G Species: Ratus norvegicus (Norawy rat)

[C Species: A 3342; A90937; R02143

[C Species: A 3342; A90937; A 3342; A 342; A 343; A 34

Gaps . 0 / Match B4.1%; Score 122; DB 1; Length 429; Local Similarity 95.7%; Pred. No. 4.1e-10; Local 22; Conservative 0; Mismatches 1; Indels Query Match Best Local S Matches 22

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# 2 GEGYQSRVDHPHFPKPIVRSITK 24 ð

284 GEGYQCRVDHPHFPKPIVRSITK 306 g

RESULT 2

Ige chain C3 region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: O2-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: 168730
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid A;Reference number: 1544443; MUID:88152907; PMID:3346043

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C;Accesion: A02145

R;Tshida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.

EMBO, O. 1, 117-1123, 1982

R;Tshida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.

EMBO, O. 1, 117-1123, 1982

A;Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison w A;Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison w A;Reference number: A90966; MUID: 84236092; PMID: 6329728

A;Reference number: A90966; MUID: 84236092; PMID: 6329728

A;Reference number: A03045

A;Reference number: A03046

A;Reference number: A03046

A;Residues: 1-423 < ISH>
A;Residues: 1-423 < ISHP
A;Residues: 1-423 
                                                                                                                                                                                             S38864
Ig epsilon chain C region - mouse (fragment)
C;Species Ma musculus (house mouse)
C;Species Ma musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C;Accession: S38864
R;Kibpy, B.; Becker, W.; Schlaak, M.
Submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of A;Recession: S38864
A;Accession: S38864
A;Accession: S38864
A;Status: preliminary
A;Molecule type: mRNA
A;Restations: L-548 «KIP-
A;Cross-references: EMBL:227397; NID:9416537; PIDN:CAA81788.1; PID:9940782
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology < IMM>
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C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: I36648
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     247 GYGYQCIVDHPDFPKPIVRSITK 269
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C;Species: Mus musculus (house mouse)
C;Accession: A02144
R;Liu, F:I; Albrandt, K.; Sutcliffe J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7882-7886, 1892
A;Title: Cloning and nuclectide sequence of mouse immunoglobulin epsilon chain cDNA.
A;Reference number: A02144; MUID:83117774; PMID:6818553
A;Title: Cloning and nuclectide sequence of mouse immunoglobulin consists
A;Residues: 1-388 «LIU»
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap hain disulfide bonds. In mome cases, such as IgA and IgM, the subunits associate into la C;Complex: An immunoglobulin c region; immunoglobulin homology (fragment)
C;Complex: An immunoglobulin homology (fragment)
F;144/Domain: immunoglobulin homology (IM2»
F;81-149/Domain: immunoglobulin homology (IM3»
F;20-361/Domain: immunoglobulin homology (IM4»
F;20-361/Domain: immunoglobulin homology (IM4»
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-107 <RBS-
A,Residues: 1-107 <RBS-
A,Cross-references: GBENZ2933; NID:g194464; PIDN:AAA37915.1; PID:g194469
C,Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 82.6<sup>1</sup>
Matches 19, Conservative
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les 19; Conservative
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Gaps

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A;Molecule type: protein
A;Molecule type: protein
A;Moseiduse: 'GAMTL', 6'.X', 8-16,'B',18-43,'B',45-52,55-92,95-97,'B',99-121,'B',123,'L',1]
A;Experimental source: myeloma protein Nd
R;Kenten, J.H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; (
Proc. Natl. Acad. Sci. U.S.A. 79, 6661-6665, 1982
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin ep:
A;Reference number: A93933; MUID:83065234; PMID:6815656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A/Status: nucleic acid sequence not shown
A/Status: nucleic acid sequence not shown
A/Status: nucleic acid sequence not shown
A/Status: nucleic acid sequence nucleic acid sequence
A/Status: 98-352 < IKE>
B/Stang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
B/Stang, K.; Max, E.E.; Cheah, H.K.; Saxon, A.
A/Status: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produce:
A/Status: A/Status: A53116; MUID:94103254; PMID:8276835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Map position: 14032.33-14032.33
A;Introns: 1/1; 104/1; 211/1; 319/1
C;Complex: An immunoglobulin hererotetramer subunit consists of two identical light (ka hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1 C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F;22-87/Domain: immunoglobulin homology < IM.>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Purification and characterization of a recombinant human IgE Fc-epsilon fragme: A;Reference number: S02438; MUID:88083554; PMID:3121387
A;Accession: S02438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F)128-195/Domain: imminoglobulin homology <IM2>
F)232-30/Domain: imminoglobulin homology <IM3>
F)232-30/Domain: imminoglobulin homology <IM3>
F)338-407/Domain: imminoglobulin homology <IM4>
F)44/Disulfide bonds: interchain (to light chain) #status predicted
F)14/Disulfide bonds: interchain (to light chain) #status predicted
F)21-49,99,146,252,275/Binding site: carbohydrate (Asn) (covalent) #status experimental
F)21,209/Disulfide bonds: interchain (to heavy chain) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Status: preliminary
A, MoLecule type: mRNA
A, MoLecule type: mRNA
A, Residues: 320-428 < ZH2>
A, Experimental source: myeloma U266-derived cell line AF-10
A, Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
R, Hellman, L.
Eur. J. Immunol. 23, 159-167, 1993
A, Title: Characterization of four novel epsilon chain mRNA and a comparative analysis (A, Reference number: A46536; MUID:93122085; PMID:8419166
A, Accession: Q46536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Status: preliminary; not compared with conceptual translation A,Status: preliminary; not compared with conceptual translation A,Status: preliminary; not compared with conceptual translation A,Rocasidues: 382-426 (*REL.)
A,Cross-references: GB:S55273; NID:g263166; PIDN:AAB24857.1; PID:g263167
A,Rocession: D46536
A,Rocession: D46536
A,Residues: 382-391 <HB2>
A,Residues: 382-391 <HB2>
A,Gross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
A,Residues: 382-391 <HB2>
A,Gross-references: GB:S55276; NID:g263168; PIDN:AAB24858.1; PID:g263169
A,Rocession: A46536
A,Rocession: A46536
A,Residues: 401-428 <HB3>
A,Gross-references: GB:S5497; NID:g263162; PIDN:AAB24855.1; PID:g263163
A,Residues: 401-428 <HB3>
A,Gross-references: GB:S5497; NID:g263162; PIDN:AAB24855.1; PID:g263163
A,Rocession: Affice: sequence extracted from NCBI backbone (NCBIP:123483)
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                                                                                                                                                                                                                                                                                                                                 A;Molecule type: mRNA
A;Residues: 1-40;68-114;427-428 <KEN>
A;Cross-references: GB:L00022; NID:g185035
R;Tkeyama, S.
FEBS Lett. 224, 306-310, 1987
                                   A;Residues: 1-356,'L', 360-428 cMAX>
A;Cross-references: GB:J00222; NID:g184755
A;Cross-references: GB:J00222; NID:g184755
A;Note: this sequence difference may be due to polymorphism
F;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.
In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-3
A;Reference number: A94418
A;Accession: A94418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig epsilon chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31.Mar-1981 #sequence revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession A22771; A23195; FH1214; A93491; A90824; A94418; B93933; S02438; A53116; C46
R;Flanagan, J.G.; Rabbitts, T.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A22771
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: 1-428 cFLA>
A;Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:g185035
R;Ucda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Honjo, T.
BRDO J. 1, 1539-1544, 1982
A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudog A;Reference number: A23195; MUID:84207910; PMID:6327276
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A;Residues: 2-428 <UED.
A;Cross-references: GB:J00222; NID:g184755
R;Zhang, K.; Saxon, A.; Max, E.E.
B;Zhang, K.; Saxon, A.; Max, E.E.
A;Zhang, K.; Saxon, A.; Max, E.E.
A;Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicing
A;Reference number: PH1214; MUID:92308839; PMID:1613458
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A,Residues: 320-428 <ZHA>
A,CROS-STEACHOCSS: 320-428 KERL:X63693, GB:S38668; NID:g32987
A,CROS-STEACHOCSS: BMEL:X63693, GB:S38668; NID:g32987
R,SENO. M.; KUTOKAWA, T.; Ono, Y.; Onda, H.; Sasada, R.; Igarashi, K.; Kikuchi, M.; Sugi
Nucleic Acids Res. 11, 719-726, 1983
Nucleic Acids Res. 11, 719-726, 1983
A,Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon cha
A,Reference number: A93491; MUID:83168897; PMID:6300763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBO J. 1, 655-660, 1982
A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gene
A;Reference number: A22771; MUID:84236029; PMID:6234164
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A; Residues: 1-428 <SEN>
A; Cross references: Bill00022; GB:J000227; GB:V00555; NID:g185035
A; Cross references: GB:L00022; GB:J00227; CB:V00555; NID:g185035
Cell 29, 691-699; 1982
A; Title: Duplication and deletion in the human immunoglobulin epsilon genes.
A; Reference number: A90824; MUID:83001945; PMID:6288268
A; Accession: A90824
A; Molecule type: DNA
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Best Local Similarity 65.2%; Pred. No. 0.00022;
Matches 15; Conservative 2; Mismatches 6; Indels
        Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
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55.2%; Score 80; DB 1; Length 428

Query Match

Best Loc Matches

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A; Molecule type: DNA
A; Mesidues: 1.345 cKRO>
A; Gross-references: GBN31012
R; Guillemot, F.; Billault, A.; Pourquie, O.; Behar, G.; Chausse, A.M.; Zoorob, R.; Krei.
EMBO J. 7, 2775-2785, 1988
A; Title: A molecular map of the chicken major histocompatibility complex: the class II
A; Reference number: S01172; MUID:89030642; PMID:3141149
                                           A;Residues: 1-264 <SYH>
A;Residues: 1-264 <SYH>
A;Cross-references: EMBL:X33054; NID:957169; PIDN:CAA37221.1; PID:957170
C;Across-references: EMBL:X33054; NID:957169; PIDN:CAA37221.1; PID:957170
C;Superfamily: class II histocompatibility antigen, immunoglobulin horloopy
C;Reywords: glycoprotein; heterodimer; transmembrane protein
C;Reywords: glycoprotein; heterodimer; transmembrane protein
F;126/Domain: signal sequence #status predicted <SIG>
F;27-264/Product: class II histocompatibility antigen, RTI-D beta-I chain #status predicted
F;137-202/Domain: immunoglobulin homology <IRM>
F;229-246/Domain: transmembrane #status predicted <IRM>
F;46/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Cross-references: EMBL:X12780; NID:g63089; PIDN:CAA31272.1; PID:g63080
A;Cross-references: EMBL:X12780; NID:g63089; PIDN:CAA31272.1; PID:g63080
C;Genetics: 16
C;Guperfamily: class I histocompatibility antigen; immunoglobulin homology
C;Superfamily: class I histocompatibility antigen Brotein
F;1-22/Domain: aignal sequence #status predicted cSIG>
F;23-345/Porduct: class I histocompatibility antigen Br IV alpha chain #status predict F;23-110/Domain: alpha-1 cEXT1>
F;23-110/Domain: alpha-1 cEXT2>
F;211-201/Domain: alpha-1 cEXT2>
F;211-201/Domain: immunoglobulin homology cIMM>
F;32-345/Domain: irransmembrane #status predicted cIMM>
F;32-345/Domain: intracellular #status predicted cIMM>
F;32-345/D
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C;Species: Gallus gallus (chicken)
C;Accession: 151309
R;Fulton, J.E.; Thacker, E.L.; Bacon, L.D.; Hunt, H.D.
Eur. J. Immunol. 25, 2069-2076, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Gallus gallus (chićken)
C;Date: 30-Jun-1992 #seguence_revision 30-Jun-1992 #text_change 22-Jun-1999
C;Accession: A45846; S01172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHC class I histocompatibility antigen B-F IV alpha chain precursor
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Immunogenetics 31, 405-409, 1990
A;Title: Structure and expression of a chicken MHC class I gene.
A;Reference number: A45846; MUID:90316612; PMID:2370087
A;Accession: A45846
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.2%; Score 51; DB 2; Length 264;
larity 47.1%; Pred. No. 6.6;
Conservative 3; Mismatchés 6; Indels
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Matches 8; Conservative
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Best Local Similarity
Matches 8; Conserv
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HLCHB4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEC class II E-beta protein - rat (fragment)

Cispecies: Rattus norvegicus (Norway rat)

Cispecies: Rattus norvegicus (Norway rat)

Cispecies: Rattus norvegicus (Norway rat)

Cispecies: Astrus norvegicus (Norway rat)

Cispecies: Astrus norvegicus (Norway rat)

Cispecies: Astrus norvegicus (Norway rat)

Cispecies: Ascoberson: ISS951

Michaele (Norway rat)

Michaele 
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H-2 class II histocompatibility antigen RT1.D-mu beta chain precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 21-Jan-2000
C;Accession: A60497
E;Holowachuk, E. M.; Greer, M.K.
Diabetes 38, 267-271, 1989
A;Title: Unaltered class II histocompatibility antigens and pathogenesis of IDDM in BB: A;Reference number: A60497; MUID:89121214; PMID:2464510
A;Accession: A60497, MUID:89121214; PMID:2464510
A;Accession: A60497, MUID:89121214; PMID:2464510
A;Accession: A60497
A;A
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510989
510989
Class II histocompatibility antigen RT1-D beta-I chain precursor - rat
Cjspecies: Rattus norvegicus (Norway rat)
Cjspecies: Rattus norvegicus (Norway rat)
Cjspecies: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 21-Jan-2000
Cjspecession: S10989
Riskha-Jedelhauser, J.; Reske, K.
Nucleic Acids Res. 18, 4598, 1990
AjTitle: Sequence of rat cDNA clone pLR-beta-112 coding for the RT1.D-beta' chain.
AjReference number: S10989; MUID:90356406; PMID:2388838
AjAccession: S10989
AjAccession: S10989
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C.Superfamily: class II histocompatibility antigen; immunoglobulin homology
F;137-202/Domain: immunoglobulin homology <IMM>
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47.1%; Pred. No. 6.6;
iive 3; Mismatches
                                                 Pred. No. 0.00
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GEVYTCQVEHPSLPSPV 211
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Matches 8; Conservative
                                                 Local Similarity 60.9%;
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A;Title: Functional analysis of avian class I (BFIV) glycoproteins by epitope tagging an A;Reference number: 151309, MUID:95347411; PMID:7621880
A;Accession: 151309
A;Accession: 151309
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-355 <FULD.
A;Cross-references: GB:S78682; NID:gl042200; PIDN:AAB34945.1; PID:gl042201
C;Genetics:
A;Gene: BFIV21
C;Genetics:
A;Gene: BFIV21
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;213-278/Domain: immunoglobulin homology <IMM>
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R;Milne, S.; Kaufman, J.; Beck, S.
submitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility compl
A;Reference number: 220475
A;Accession: T28149
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R;Milne, S.; Kaufman, J.; Beck, S.
Ribmitted to the EMBL Data Library, May 1998
A;Description: DNA sequencing and analysis of the chicken major histocompatibility compl
A;Reference number: 220475
A;Accession: T28152
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T28152
MHC Class I histocompatibility antigen B-F IV alpha chain precursor - chicken
C;Species: Gallus gallus (chicken)
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHC class I histocompatibility antigen B-F alpha chain 2 - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
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A,Introns: 22/1; 110/1; 201/1; 292/1; 328/1; 339/1; 350/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Introns: 22/1; 110/1; 201/1; 292/1; 328/1; 339/1; 350/1
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
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A;Cross-references: EMBL:AL023516; PIDN:CAA18972.1
A;Experimental source: clone cB12
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A;Cross-references: EMBL:AL023516; PIDN:CAA18969.1
A;Experimental source: clone cB12
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Best Local Similarity 50.0%; Pred. No. 18;

Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 GEGYQSRVDHPFFKP 17

Db 271 GDKYQCRVEHASLPQP 286

Search completed: February 26, 2004, 08:28:14 ...

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1 CGEGYOSRVDHPHFPKPIVRSITKC 25
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WROTI CABEL
GCI MOUSE
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GCIM MOUSE
GCA MAT
GHIT HUMAN
VNST CVBG
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44	44	44	44	44	43.5	43.5	43.5	43.5	43	43	43	
34	33	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

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MEDINE-82174576; PubMed=6803238;

MEDINE-82174576; PubMed=6803238;

MEDINE-82174576; PubMed=6803238;

MEDINE-82174576; PubMed=6803238;

MEDINE-82174576; PubMed=6803238;

MEDINE-82174576; PubMed=6803238;

The limit of rat immunoglobulin E.";

Proc. Natl. Acad. Sci. U.S. A. 79:1264-1268 (1982).

L. Froc. Natl. Acad. Sci. U.S. A. 79:1264-1268 (1982).

L. Froc. Natl. Acad. Sci. U.S. A. 79:1264-1268 (1982).

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                                                                                              21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Ig epsilon chain C region.
Rattus norvegicus (Rat)
Bukaryota, Merazoa; Chorcata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                         STRAIN=LOU/C/WSL;
MEDLINE=2056453;
MEDLINE=2056453;
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
"Structure and evolution of the heavy chain from rat immunoglobulin
"Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                             [2]

SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).

MEDLINE=83182019; PubMed=6820340;

Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;

Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;

A cloned cDNA probe for rat immunoglobulin epsilon heavy chain:

"A cloned cDNA probe for and DNA sequence.";

DNA 1:335-343(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Immunoglobulin domain; Immunoglobulin C region; Repeat.
                                       429 AA
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2)
                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids Res. 10:6041-6049(1982)
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                                                                               21-JUL-1986 (Rel. 01, Created)
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 3.
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InterPro, IPR007110, Ig-like.
InterPro, IPR003597, Ig cl.
InterPro, IPR003006, Ig MHC.
                                         STANDARD;
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                                                                                                                                                                                                                                NCBI_TaxID=10116;
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RESULT 1
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261
365
415
421 AA;
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P01854;
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                                                       DISULFID
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                                                                                               CARBOHYD
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MEDLINE-84236092; PubMed-6329728;
IShida N., Ueda S., Hayashida H., Miyata T., Honjo T.;
Thida C., Ueda S., Hayashida H., Miyata T., Honjo T.;
The nuclectide sequence of the mouse immunoglobulin epsilon gene:
comparison with the human epsilon gene sequence.";
EMBO J. 1:1117-1123 (1982).
                                                                                                                                                                                                                                                                                                                                        EPC_MOUSE STANDARD; PRT; 421 AA.
P06336; P01856;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 epsilon chain C region.
Buts muscalus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euteleostomi; Mammalia; Euteleostomi; Marmalia; Euteleostomi; Marmalia; Euteleostomi; Muridae; Murinae; Mus.
1717 TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 34-421 FROM N.A. WEDLINESS11, WEDLINESS11774; PubMed-6818553; Liu F.-T., Albrandt K. Sutcliffe J.G., Katz D.H.; Cloning and nucleotide sequence of mouse immunoglobulin epsilon
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InterPro; IPR0030110; Ig-like.
InterPro; IPR003006; Ig C1.
InterPro; IPR003006; Ig MHC.
Pfam; PF00047; ig; 4.
SMART; SMO407; IG: 12.
PROSITE; PS50815; IG LIKE; 4.
PROSITE; PS00290; IG MHC; 3.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
                                                                                                                                                 Score 122; DB 1; Length 429; Pred. No. 3.2e-10; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Honjo T.;
Submitted (APR-1986) to the EMBL/GenBank/DDBJ databases
                                                                                                             D2970B34EF8A72B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).
IG-LIKE 1.
IG-LIKE 2.
IG-LIKE 3.
IG-LIKE 4.
R -> N (IN REF. 2).
P -> L (IN REF. 2).
                                                                                                                                                                   Pred. No. 3.26
0; Mismatches
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888
                                                                                                               48671 MW;
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Best Local Similarity 95.7%;
Matches 22; Conservative
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PIR; A02145; EHMSS.
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103
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429 AA;
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PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND).
Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
(In) Bach M.K. (eds.);
Immediate hypersensitivity: modern concepts and developments, pp.1-36,
[6]
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MEDLINE-83001945; PubMed-6288268;
Max E.B., Bartey J., Ney R., Kirsch I.R., Leder P.;
Induplication and deletion in the human immunoglobulin epsilon genes.";
Cell 29:691-699(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDIATE=8916889; PubMed=6300763;
Seno M., Kurokawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
"Molecular cloning and nucleotide sequencing of human immunoglobulin
epsilon chain cDNA ";
Nucleic Acids Res. 11:719-726(1983).
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Flanagan J.G., Rabbitts T.H.;
"The sequence of a human immunoglobulin epsilon heavy chain constant
region gene, and evidence for three non-allelic genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Honjo T.;
human immunoglobulin
                                                                                                                  (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                             Score 98; DB 1; Length 421;
Pred. No. 9.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                       4; Indels
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8F909E1F30A06B47 CRC64;
CH4.

BY SIMILARITY.

BY SIMILARITY.

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BY SIMILARITY.

N-LINKED (GLCNAC...)

N-LINKED (GLCNAC...)
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
IGHE.
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                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epsilon pseudogene that lacks introns.";
EMBO J. 1:1539-1544(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 GYGYQCIVDHPDFPKPIVRSITK 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 GEGYQSRVDHPHFPKPIVRSITK 24
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84 884
95 166
6 238
263 261
415 415
47320 MW;
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82.6%;
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Nucleic Acids Res. 18:4598-4598(1990).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-Lewis familiaris; TISSUE-Bone marrow;
MEDLINE-90356406; PubMed-2388838;
Syha-Jedelhauser J., Reske K.;
"Sequence of rat cDNA clone plR beta 112 coding for the RTI.D beta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
RTI class II histocompatibility antigen, D-1 beta chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.2%; Score 80; DB 1; Length 428; llarity 60.9%; Pred. No. 0.00038; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47019 MW; 25C4CA072AA558A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            294 GETYQCRVTHPHLPRALMRSTTK 316
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  418
428 AA;
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les 14; Conserv
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SEQUENCE
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                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A. MEDLINE-83065234; PubMed=6815656; Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J. Bell L.O., Gould H.J.; element of the gene for the human immunoglobulin egeinon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                                     R GO; GO:0003823; F:antigen binding; NAS.

R GO; GO:0003825; P:immune response; NAS.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003006; Ig_MHC.

R Pfam; PF00047; Ig; 4.

R PROSITE; PS00290; IG_MHC; 3.

R PROSITE; PS00290; IG_MHC; 3.

R Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; NON_TER.

NON_TER.
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M -> L (POSSIBLE POLYMORPHISM).
/FITIG=VAR_003885.
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IG-LIKE 2.
IG-LIKE 3.
IG-LIKE 4.
INTERCHAIN (WITH A LIGHT CHAIN)
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                                                                                               3D-STRUCTURE MODELING.
MEDLINE=87089848; PubMed=3796618;
Radlan E.A., Davies D.R.;
"A model of the For immunoglobulin E.";
Mol. Immunol. 23:1063-1075[1986].
-1- SIMILARITY: Contains 4 immunoglobulin-like domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERCHAIN
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                                                                                                                                                                                                                                                                                            PDB; 1128; 15-011-92.
PDB; 1FP5; 30-7AN-02.
PDB; 1G84; 16-MAY-01.
PDB; 100V; 18-SEP-02.
Genew; HGNC: 5522; IGHE.
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MEDLINE=89030642; PubMed=3141149;
MEDLINE=89030642; PubMed=3141149;
Guillemot F., Billault A., Pourquie O., Behar G., Chausse A.M.,
Zoorob R., Kreibich G., Auffray C.;
"A molecular map of the chicken major histocompatibility complex: the class II beta genes are closely linked to the class I genes and the mucleolar organizer.";
EMBO J. 7:2775-2785(1988).
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01-APR-1990 (Rel. 14, Last sequence update)
15-UUL-1999 (Rel. 38, Last annotation update)
15-UUL-1999 (Rel. 38, Last annotation update)
16-UUL-1999 (Rel. 38, Last annotation update)
16-UUL-1999 (Rel. 38, Last annotation)
16-Uule gallus (Chicken)
16-Procentaling gallus (Chicken)
17-Procentaling (Procentaling Chicken)
18-Procentaling (Procentaling Chicken)
18-Procentaling (Procentaling (Pro
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BY SIMILARITY.

N-LINKED (GLCNAC. . .) (FOTENTIAL)

1587357355177DA1 CRC64;
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EXTRACELLULAR BETA-1.
EXTRACELLULAR BETA-2.
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                                                                                                                                                                                                                                                                                  HSSP, E13760, 2SEB.
InterPro; IPR00159; Ig-like.
InterPro; IPR00359; Ig_c1.
InterPro; IPR00359; Ig_c1.
InterPro; IPR00359; Ig_c1.
InterPro; IPR00359; MHC_II_beta.
Pfam; PF0047; ig; I._beta; I.
ProDom; PF00047; ig; I._beta; I.
SMART; SM00407; IGC1; I._beta; I.
PROSITE; PS50835; IG_LIKE; I.
PROSITE; PS00290; IG_MHC; I.
MHC II; Transmembrane; Glycoprotein; Signal.
SIGNAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
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Kroemer G., Zoorob R., Auffray C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEVYTCQVEHPSLPSPV 211
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                                                                                                                                                                                                                                       EMBL; X53054; CAA37221.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 47.1 nes 8; Conservative
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                                                                                                                                                                                                                                                                       PIR; S10989; S10989.
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DISULFID
CARBOHYD
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TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEJ outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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0
"Structure and expression of a chicken MHC class I gene.";
Immunogenetics 31:405-409(1990).
-!- FUNCTION: Involved in the presentation of foreign antigens to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASS I HISTOCOMPATIBILITY ANTIGEN, F10
                                                                                                    SUBUNIT: Heterodimer of an alpha chain and a beta chain (beta-2-microglobulin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-GT-2003 (Rel. 42, Last amoutation update)
UDP-N-accetylmuramcylalanyl-D-glutamate--2,6-diaminopimelate ligase
(EC 6.3.2.13) (UDP-N-accetylmuramyl-tripeptide synthetase) (Meso-diaminopimelate-adding enzyme) (UDP-MurNAc-tripeptide synthetase)
WURB-OR FN1225.
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BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
P -> PDREGGSSSST (IN REF. 2).
W; 430DCCF8091B69A4 CRC64;
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50.0%; Pred. No. 9.2;
iive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
CONNECTING PEPTIDE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pram; PP00129; MHC I; 1.
PRINTS; PR01638; MHCCLASSI.
Probom; PD000050; MHC I; 1.
PR0SITE; SM00407; IGGI; 1.
PROSITE; PS00290; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, X12780; CAA31272.1; --
EMBL, M31012, AAA48947.1; --
PIR, A45846; HLCH84.
HSSP, P13599; 3FRU.
InterPro; IPR00310; Ig-like.
InterPro; IPR003506; Ig_MIC.
InterPro; IPR003006; Ig_MIC.
InterPro; IPR003006; Ig_MIC.
PEam; PF00047; ig; 1.
PEam; PF00129; MIC_I: 1.
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272 GDKYQCRVEHASLPQP 287
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SIGNAL 1 22
CHAIN 23 345
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Best Local Similarity
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                                                                                           immune system.
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                                                                                                                     -!- SUBUNIT:
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QBR635;
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CONFLICT
SEQUENCE
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REVISIONS.
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (By similarity).

-!- CATALYTIC ACTIVITY: ATP + UDP-N-acetylmuramoyl-1-alanyl-D-glutemate+ meso-2,6-diaminoheptanedioate = ADP + phosphate + UDP-N-acetylmuramoyl-1-alanyl-D-gamma-glutamyl-meso-2,6-diaminoheptanedioate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Bristol N2;
MEDLINE=59387388; bubMed=7658466;
MEDLINE=59387388; bubMed=7658466;
Sano T., Tabuse Y., Nishiwaki K., Miwa J.;
"The tpa-1 gene of Caenorhabditis elegans encodes two proteins similar to Ca(2+)-independent protein kinase Cs: evidence by complete genomic and complementary DNA sequences of the tpa-1 gene.";
J. Mol. Biol. 251:477-485(1995).
                              MEDLINE=21886394; PubMed=11889109; Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Kapatral V., Anderson I., Ivanova N., Garchkin G., Zhu L., Ushattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Gensein M., Kyrpides N., Overbeek R., "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum Errain ATCC 25586."

J. Bacteriol. 184:2005-2018(2002).

-- FUNCTION: Cell wall formation. Diaminopimelic acid adding enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1994 (Rel. 28, Created)
01-FEB-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Protein kinase C-like 1 (EC 2.7.1.-) (FKC) (Tetradecanoyl phorbol acetate registant protein 1).
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InterPro; IPR000713; Mur_ligase.
InterPro; IPR004101; Mur_ligase_C.
InterPro; IPR005761; MurE.
InterPro; IPR005761; MurE.
Pfam; PP01225; Mur_ligase_C; 1.
IGRFAMS; TIGR01085; murE, 1.
ATP-binding; Complete proteome.
NP_BIND
IOS IN ATP (COMPLET) IN ATP (COM
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485 AA; 55484 MW; E6299E43F2B7FF19 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY: Peptidoglycan biosynthesis.
SUBCELDIAR LOCATION: Cytoplasmic (Probable).
SIMILARITY: Belongs to the murCDEF family.
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les 9; Conservative
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SOLUTION SOL
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ALTERNATIVE PRODUCTS:
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DOMAIN
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Transferase; Serine/threonine-protein kinase; ATP-binding; Zinc;
Photbol-ester binding; Repeat; Alternative splicing; Phosphorylation.
DOMAIN 138 287 PHORBOL-ESTER AND DAG BINDING 1.
DOMAIN 238 287 PHORBOL-ESTER AND DAG BINDING 2.
DOMAIN 315 34 PROTEIN KIRASE.
BINDING 404 404 ATP (BY SIMILARITY).
BINDING 404 404 ATP (BY SIMILARITY).
ACT SITE 499 BY SIMILARITY).
MOD RES 89 PHOSPHORYLATION (AUTO-) (POTENTIAL).
MOD RES 324 PHOSPHORYLATION (AUTO-) (POTENTIAL).
MOD RES 324 PHOSPHORYLATION (AUTO-) (POTENTIAL).
MARSFLIC 1 137 MISSING (in isoform b).
// FTIG-VSP_004744.
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MEDINE=80012837; PubMed=113776;
MEDINE=8012837; Clarke P., Salesr W.;
"Sequence analysis of cloned cDNA encoding part of an immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=80202559; PubMed=6769752;
Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Saidman J.G., Peterlin B.M., Leder P., Honjo T.;
"Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid.";
Gene 9:87-97(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
16 gamma-1 chain C region secreted form,
18 wms musculus (Mouse).
Enkaryota, Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
11 TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINES 80045036; PubMed=115593;

Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,

Takahashi N., Mano Y.;

Takahashi N., Mano Y.;

Geling and complete nucleotide sequence of mouse immunoglobulin

gamma 1 chain gene.";

Cell 18:559-568(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFIDE BONDS (MOPC 21).
MEDLINE=73008889; PubMed=5073237;
Svafti J., Milstein C.;
Svafti J., Milstein C.;
"The disulphide bridges of a mouse immunoglobulin G1 protein.";
Blochem. J. 126:837-850(1972).
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                                                                                                                                                                                                                                                                                              C44F2E25F58057E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE (MYELOMA PROTEIN MOPC 21).
MEDLINE=78242288; Pubmed=98524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
                                                                                                                                                                                                                                                                                                704 AA; 80298 MW;
                                                                                                                                                                                                                                                                                                                                      33.4%;
ilarity 37.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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hes 11; Conserv
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P01868;
                                                                                                                                                                                                                                                                                                SEQUENCE
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GC1 MOUSE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BYML outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GCIM_MOUSE
AC PO1865.
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-AUG-1991 (Rel. 142, Last annotation update)
DT 00-CT-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 10-Mamma-1 chain C region, membrane-bound form.
OC Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
OC Mamma-lia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
OC NCBI_TAXID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN)
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N -> D (IN REF. 3).
MW; A338812F3D1F2C93 CRC64;
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Event=Alternative splicing; Named isoforms=2;
Name=Secreted;
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                                                                                 Isold=P01868-1; Sequence=Displayed;
Note=May be the major isoform;
Name=Membrane-bound;
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193 GKEFKCRVNSAAFPAPIEKTISK 215
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InterPro; IPR003597; Ig_c1.
InterPro; IPR00306; Ig_MHC.
Pfam; PF00047; ig; 2.
SMART: SM0407; Ig0. 2.
PROSITE: PS50835; IG_LIKE; 3.
PROSITE; PS00299; IG_MHC; 1.
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EMBL; V00793; CAA24173.1; --
EMBL; V00793; CAA24174.1; --
EMBL; V00793; CAA24175.1; --
EMBL; V00795; CAA24175.1; --
EMBL; V00795; CAA24176.1; --
EMBL; V00795; CA
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324 AA;
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MEDLINE=82222190; PubMed=6283537;

Wamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;

"Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";

Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

-i. ALTERNATIVE PRODUCTS:

EVent-Alternative splicing; Named isoforms=2;
[1]
SEGUENCE FROM N.A.
MEDLINE=80045036; PubMed=115593;
Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
Takahashi N., Mano Y.;
Groning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene.";
Cell 18:559-568(1979).
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0
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SEQUENCE OF 323-393 FROM N.A.
MEDILINE=82197626; PubMed=6804950;
Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.
"mRNA for surface immunoglobulin gamma chains encodes a highly
conserved transmembrane sequence and a 28-residue intracellular domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 323-366 FROM N.A. MEDINE-8211-525; PubMed=6799207; MEDINE-8211-525; PubMed=6799207; Mogrs J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.; Insumerate D., Wall R.; Insumerate encoding transmembrane carboxyl termini of immunoglobulin gamma chains."; Cell 26:19-27(191)
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NON IER 1 1 97 CH1.
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PDB; 15C8; 23-MAR-99
PDB; 1AC8; 18-MAR-99
PDB; 1CL7; 12-JAN-00
PDB; 1E11; 06-FEB-01
PDB; 1KC5; 24-JUL-02
PDB; 1KC5; 24-JUL-02
PDB; 1KC5; 24-JUL-02
PDB; 1KC7; 11-MAY-02
PDB; 1KC8; 10-MAY-02
PROSTIE; PSS0835; 1G LIKE; 3.
PROSTIE; PSS0835; 1G LIKE; 3.
PROSTIE; PSS0835; 1G LIKE; 3.
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EMBL, V00793; CAA24173.1; -.
EMBL; V00793; CAA24174.1; -.
PIR; B02159; GIMSM.
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217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                 Gaps
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HEAVY CHAIN).
HEAVY CHAIN).
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Pred. No. 15;
7; Mismatches 7; Indels
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                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
4CC88343B7A1CE27 CRC64;
                                  INTERCHAIN (WITH A LIGHT INTERCHAIN (WITH A HEAVY INTERCHAIN (WITH A HEAVY INTERCHAIN (WITH A HEAVY
                                                                                                                                      N-LINKED (GLCNAC. . .).
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01-FEB-1991 (Rel. 17, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
13 gamma-2A chain C region.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 AA
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IG-LIKE 2.
IG-LIKE 3.
                                                                                                                                                                          POTENTIAL.
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PIR; PS0019; PS0019.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig.cl.
InterPro; IPR030067; Ig.MHC.
Pfan; PP00047; ig. 2.
SMART; SM00407; IGC1; 2.
                                                                                                                                                                                                                     43386 MW;
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PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
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39.1%;
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NON TER 1 1
DOMAIN 6 98
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221
221
102
105
105
136
242
172
322 AA;
                                                                                                                                                                                                                                                                            Local Similarity
es 9, Conserv
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                                                                                                                                                                                                                     393 AA;
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Matches
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                          Gaps
                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                   Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S., Ansorge W., Boecher M., Bloecker H., Bauersachs S., Blum H., Lauber J., Duestenhoeft A., Beyer A., Koehrer K., Strack N., Mewes H. W., Ottenwelder B., Obermaier B., Tampe J., Heubner D., Wambutt R., Korn B., Klein M., Poustka A., "Twape J., Heubner D., Manutt R., Korn B., Klein M., Poustka A., and Janalysis of Actalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs."; Genome Res. 11:422-435 (2001).
                          ..
0
       Query Match 32.4%; Score 47; DB 1; Length 322; Best Local Similarity 39.1%; Pred. No. 17; Matches 9; Conservative 7; Mismatches 7; Indels
                                                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUB-Dermal papilla;
Iseda A., Yamashita M., Yoshimoto M.;
"Molecular cloning of a dermal papilla derived gene.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Mei G., Yu W., Gibbs R.A.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                               Mao Y.M., Xie, Y., Mu Z.M., Li Y., Huang Y.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                        345 AA.
                                                     | ::::|: | | | | :|:|
191 GKTFKCKVNSGAFPAPIEKSISK 213
                                           GEGYOSRVDHPHFPKPIVRSITK 24
                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Kidney;
MEDLINE=21154917; PubMed=11230166;
                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                     SHITM OR DERP2
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HUMAN
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STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=96337999; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou i., Fleischmann R.D.,
Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberte K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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human and mouse cDNA sequences.";
proc. NaI. Acad. Sci. U. S.A. 99:16899-16903(2002).
-!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: Belongs to the B11 family.
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Pred. No. 21;
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E -> G (IN REF. 3).
I -> M (IN REF. 4).
Q -> R (IN REF. 4).
A : BOBFAED86A9CD98E CRC64;
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Archaea; Euryarchaeota; Methanococci; Methanococcales;
Methanocaldococcaceae; Methanocaldococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOR METUA STANDARD; PRT; 116 AA. 058151; DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation update) Putative superoxide reductase (EC 1.15.1.2) (SOR).
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60
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EMBL; AF131820; AAD20052.1; -.
EMBL; AF060923; AAG43135.1; -.
EMBL; AL136713; CAB66648.1; -.
EMBL; BC010354; AAH10354.1; -.
Genew; HGNC:17281; GHITM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37205 MW;
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Pfam; PF01027; UPF0005; 1.
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51.9%;
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146
180
211
234
265
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74
118
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345 AA;
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126
160
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214
272
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Best Local
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277 AA; 31896 MW;
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                                                                                                                                                                                                              GCB MOUSE
                             Query Match
Best Local {
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                                                                                                                              78
 SEQUENCE
                                                                Matches
                                                                                                 à
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                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Cox G.J., Parker M.D., Babluk L.A.,
"The sequence of CDNA of bovine coronavirus 32K nonstructural gene.";
Nucleic Acids Res. 17:5847-5847(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
TO CATALYZE THE REDUCTION OF SUPEROXIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bovine coronavirus (frain Quebec) (BCOV) (BCV).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
               HYDROGEN PEROXIDE (BY SIMILARITY).

CATALYTIC ACTIVITY: Reduced rubredoxin + superoxide + 2 H(+)
                                                                                                                                                                                                                                                                                                     Interpro; IPR002742; Desulfoferrodox.
Pfam; PF01880; Desulfoferrodox; 1.
Probom; PD006618; Desulfoferrodox; 1.
TIGREAMS; TIGR00332; neela ferrous; 1.
Hypothetical protein; Oxidoreductase; Electron transport; Iron;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö

    rubredoxin + H(2)0(2).
    -!- COFACTOR: Iron (By similarity).
    -!- SIMILARITY: Belongs to the desulfoferrodoxin family.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4CF2C76237DE0673 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          IRON (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 AA.
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4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.7%; Score 46;
43.5%; Pred. No. 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X15445; CAA33485.1; -.
PIR; A34039; MNIH32.
InterPro; IPR007878; Corona_NS2A.
Pfam; PF05213; Corona_NS2A; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           20 IR
46 IR
52 IR
101 IR
13950 MW;
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                                                                                                                                                                                                                            EMBL; U67520; AAB98735.1; -. PIR; E64392; E64392.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               Complete proteome.
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10-OCT-2003
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Isode=P01866-1; Sequence=Displayed;
Note=May be the major isoform;
Name=Membrane-bound;
Isold=P01867-1; Sequence=External;
Isold=P01867-1; Sequence=External;
Isold=P01867-1; Sequence=External;
Isold=P01867-1; Sequence=External;
Isold=P01867-1; Sequence=External;
ISOLGED WITH 2 SIALIC ACID RESIDUES.
-!- PTM: DISULFIDE BONDS BY HOMOLOGY WITH OTHER IG GAMMA CHAINS.
-!- MISCELLANBOUS: The a allele sequence is shown.
-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
PIR; $25057; GZM311.
HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEGUENCE FROM N.A. (ALLELE B).
MEDLINE=82173203; PubMed=6803173;
Ollo R., Rougeon F.;
"Mouse immunoglobulin allotypes: post-duplication divergence of gamma 2a and gamma 2b chain genes.";
Nature 296:761-763(1982).
                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-80081502; PubMed=117549;
Tucker P.W., Marcu K.B., Newell N., Richards J., Blattner F.R.;
"Sequence of the cloned gene for the constant region of murine gamma 2D immunoglobulin heavy chain.";
Science 206:1303-1306 (1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.; "Structure of the constant and 3' untranslated regions of the murine gamma 2b heavy chain messenger RNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ALLELE A).
MEDLINE-80120716; PubMed-6766534;
Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
Complete nucleotide sequence of immunoglobulin gamma2b chain gene
cloned from newborn nouse DNA.";
Nature 283:786-789(1980).
                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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MEDUINE-94216359; PubMed=7512667;

Kim H., Yamaguchi Y., Masuda K., Matsunaga C., Yamamoto K.,

Kim T., Yamaguchi Y., Mato K., Arata Y.;

"O-glycosylation in hinge region of mouse immunoglobulin G2b.";

"O-glycosylation in hinge region of mouse immunoglobulin G2b.";

"I Biol. Chem. 269:12345-12350(1994).

-!- SUBCELLULAR LOCATION: Secreted (Potential).
                                                                           ;
0
                                     Length 277;
                                                                           2; Indels
D2EEC7BAFB86EA11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Event=Alternative splicing; Named isoforms=2;
                                   Score 46; DB 1;
Pred. No. 20;
                                                                                                                                                                                                                                                            PO1866;
21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
11-MAR-2004 (Rel. 43, Last annotation update)
19 gamma-2B chain C region secreted form.
Mus musculus (Mouse).
                                                                                                                                                                                                                                          336 AA.
                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=80081501; PubMed=117548;
                                     31.7%;
58.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 206:1299-1303(1979)
                                                       Similarity 58.37; Conservative
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GEGFQIKFDNPH 89
                                                                                                            GEGYQSRVDHPH 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O-LINKED (GALNAC. . .).
REMOVED POST-TRANSLATIONALLY (PROBABLE).
Q -> R (IN ALLELE B).
T -> A (IN ALLELE B).
N -> D (IN ALLELE B).
N -> I (IN ALLELE B).
L -> S (IN REF. 2 AND 3).
S -> P (IN REF. 2 AND 3).
I -> T (IN REF. 2 AND 3).
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              InterPro; IPR003597; Ig_cl.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003066; Ig_MHC.
SMMART; SM00407; IG; 3.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN)
CHAIN)
CHAIN)
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16-007-2001 (Rel. 40, Last sequence update)
18-ERB-2003 (Rel. 41, Last annotation update)
Uroporphyrinogen decarboxylase (EC 4.1.1.37) (URO-D) (UPD)
SPCC4B3.05C.
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24;
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Eukaryota, Pungi, Ascomycota, Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      370 AA
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IG-LIKE 2.
IG-LIKE 3.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36658 MW;
                                                                                                                                                                                                                                                                  Alternative splicing; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 34.8%;
Matches 8; Conservative
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NCBI_TaxID=4896;
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Search completed: February 26, 2004, 08:24:21 Job time : 7.4 secs

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Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B., Goffeau E., Cadieu E., Cadieu E., Lelaure V., Mottier S., Galibert F., Aveg S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., Moreno S., Armstrong J., Forsburg S.L., The genome sequence of Schlzosaccharomyces pombe.", "The genome sequence of Schlzosaccharomyces pombe.", "Here 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -i- PATHWAY: Porphyrin and heme biosynthesis.
-i- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-i- SIMILARITY: Belongs to the uroporphyrinogen decarboxylase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- CATALYTIC ACTIVITY: Uroporphyrinogen-III = coproporphyrinogen + 4
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SEQUENCE 370 AA; 41846 MW; 110DFC463733FD89 CRC64;
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GeneDB_SPombe, SPCC4B3.05c; -.
InterPro; IPR006361; HemE.
InterPro; IPR000557; Uro_decarbxyls.
Pfam; PF01208; URO-D; 1.
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TIGRFAMs; TIGR01464; hemE; 1.
PROSITE; PS00306; UROD_1; FALSE_NEG.
PROSITE; PS00907; UROD_2; 1.
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                                                                                                            February 26, 2004, 08:18:11; Search time 31.4 Seconds (without alignments) 251.209 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Q947h4 nicotiana t
Q84071 streptococc
Q9562 trypanosoma
Q85cc4 vibrio harv
Q77pWS gallus gall
Q77pJ3 gallus gall
Q77pJ3 gallus gall
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Q95601 gallus gall
Q941p6 gallus gall
Q31400 gallus gall
Q98193 acrocephalu
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Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Stapleton M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
Champe M., Ganzalez M., Guarin H., Krommiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.;
Celniker G.JAN-2003) to the EMBL/GenBank/DDBJ databases.
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Enkaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota, Neoptera; Endopterygota, Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 42.8%; Score 62; DB 5; Length 661; Best Local Similarity 52.9%; Pred. No. 0.54; Matches 9; Conservative 3; Mismatches 5; Indels
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InterPro; IPR01876; Znf_RanGDP.
SWART; SM00547; Znf_RBZ; 1.
SROGITE; PS01358; ZF_RANBP2 1; 1.
SEQUENCE 661 AA; 72438 WW; FAE8471548E67FA4 CRC64;
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Addams M.D. Celnikers S.E., Holf R.A., Gocayne J.D.,
Addams M.D. Celnikers S.E., Holf R.A., Galle R.F.,
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Sequencing of Drosophila melanogaster genome ",
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                          Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
NCBI_TaxID=7227;
                                                                                                                               Last sequence update)
Last annotation update)
                                                    PRT; 2594 AA
                                                                                                         Created)
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Drosophila melanogaster (Fruit fly)
                                                                                              01-MAY-2000 (TrEMBLrel. 13,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                    PRELIMINARY;
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MEDINE-20196006; PubMed=10731132;

MEDINE-20196006; PubMed=10731132;

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[3]
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Bphydroidea, Drosophilidae, Drosophila.
NCBI_TAXID=7227,
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Pred. No. 2.2,
3, Mismatches 5, Indels
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Best Local Similarity 52.9
Matches 9; Conservative
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"Annotation of Drosophila melanogaster genome.",
Submitted (MAR-2000) to the EMBL/Genbank/DDBJ databases.
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PFO1485; ....,
SMART; SM00647; IBR; 1.
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PROSITE; PS0189; ZF_RING_2; 1.
PPOSITE; PS50089; ZF_RING_2; 1.
PPOSITE; PS50089; ZF_RING_2; 1.
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FlyBase, FBgn0031857; CG11321.
InterPro; IPR002867; Znf CGHC.
InterPro; IPR001876; Znf RanGDP.
InterPro; IPR001841; Znf Tring.
Pfam; PF01485; IBR; 1.
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Best Local Similarity
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S., Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kibilda Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S., "Complete genome structure of the nitrogen-fixing symbiotic bacterium
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Oryza sativa (Rice).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae;
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                            Rhizobium loti (Mesorhizobium loti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Phyllobacteriaceae; Mesorhizobium.
MCBI_TaxID=381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.2%; Score 54; DB 16; Length 317; 38.5%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mesornizobium loti.";
DNA Res. 7:331-338(2000).
DNA Res. 7:331-338(2000).
Hypothetical protein; Complete proteome.
SEQUENCE 317 AA; 33121 MW; F7DE20BB4F661F32 CRC64;
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SEQUENCE 343 AA; 36998 MW; BE4712E38FCEA175 CRC64;
                                                                                                                                                                                  01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
10-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Hypothetical protein mlr4594.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                       317 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGEGYQSRVDH----PHFPKPIVRSI 22
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=MAFF303099;
MEDLINE=21082930; PubMed=11214968;
OSJNBa0036B21.18 protein.
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                                                                                                                                       PRELIMINARY;
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ses 10; Conserva
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Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
Banzon J., An H., Baldwin D., Banzon J., Beseon K.Y., Busam D.A.,
Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
Ferriera S., Frise E., Galle R.F., Garg N.S., George R.A.,
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OUN-2003 (TrEMBLrel. 24, Last annotation update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
031846 protein.
03186. 14 OR CG18146.
01 Drosophila melanogaster (Fruit fly).
01 Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota;
02 Bukaryota, Endopterygota; Diptera, Brachycera; Muscomorpha;
03 Ephydroidea, Drosophilidae, Drosophila.
03 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
04 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
05 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
06 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
07 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
07 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
08 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
09 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
01 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
02 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
03 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
04 Insecta, Endopterygota, Diptera, Brachycera, Muscomorpha;
05 Insecta, Endopterygota, Diptera, Brachycera, Diptera, Brachycera, Br
                                        37.2%; Score 54; DB 10; Length 343; 50.0%; Pred. No. 4.8; cive 4; Mismatches 5; Indels
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Query Match
Best Local Similarity 50.07
Best Local 9, Conservative
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Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reses M.G., Spradling A., Tsang G., Wan K., Whitelaw K., Calniker S., Rubin G.M., "An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.",
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Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J., Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A., Gonfonesh T.C., Moy M., Murphy B., Nolson C., Nelson K.A., Nunoo J., Pacinesh J., Park S., Patel S., Périfer B., Scheeler F., Phouanenavong S., Pittman G.S., Puri V., Richards S., Scheeler F., Stapleton M., Strong R., Svirskas R., Tector C., Tyler D., Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.; Sequencing of Drosophila melanogaster genome.", Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Matthews B.B., Bayraktaroglu L., Campbell is Misra S., Crosby M.A., Matthews B.B., Prochnik S.E., Smith C.D., Tradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D., Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E., Tupy J.L., Drysdale R., Emmert D., Frise E., de Grey A., Harris N., Scanle S.M.J., Smith B., Shu S., Smutniak F., Mitfield E., Searle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E., "Ashburner M., Galbart W.M., Rubin G.M., Mungall C.J., Lewis S.E., Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
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Ephydroidea, Drosophilidae, Drosophila.
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FlyBase; FBGT002839; BG:DS00180.14.
InterPro; IPR0063341; DUP139.
InterPro; IPR006210; IEGF.
InterPro; IPR006210; IEGF.
Ffam, PF02363; C tripleX; 16.
SMART, SM01381; EGF 21; 6.
SEQUENCE 648 AA; 69453 MW; 3F180401F057A812 CRC64;
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STRAIN-Berkeley;
MEDLINE-99403001; Pubmed=10471707;
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Query Match
Best Local Similarity 69.20,
Best Local 9, Conservative
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NCBl_TaxID=7227;
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Q9NKD7
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Query Match
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                                                    CTRAIN-Berkeley;

A Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,

RA Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,

RA Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,

Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,

RA Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

RA Liewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,

RA Jeran L.L., Rubin G.M., Park S., Pfeiffer B., Poon L., Sequeira A.,

Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,

RA Jeran L.L., Rubin G.M., Park S., Man K.H., Weinburg T., Zhang R.,

RA Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

B. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

B. RILL AEOO3408; AFR44845.1;

DR RILL PRO052939; BG:DS00180.14.

B. InterPro; IPR006210; IEGF

DR RICHER PRO0181; BGF

DR RART; SM00181; BGF

B. ROSIISE; PS01186; BGF 2; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
George R.A., Evis S.E., Richards S. Ashburner M., Henderson S.N.,
Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Feiffer B.D.,
Abril J.F., Agbayani A., An H.J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Besson K.Y., Bence P.V., Berman B.P., Bhandari D., Bolsakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Blandari D., Bolsakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis B.,
Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burtis K.J., Evargelister C.C., Ferraz C., Ferraz S., Ferrisca S., Ferrisca M.,
Antis N.L., Farrey D., Hennan T.J., Hernandez J.R., Houck J.,
Alaris N.L., Harvey D., Hennan T.J., Hernandez J.R., Houck J.,
Alaris N.L., Harvey D., Hennan T.J., Hernandez J.R., Houck J.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liako P., Lei X., Mattei B., McIntosh T.C., McIedd M.P., Moshrefi A.,
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01-JUN-2003 (TYEMBLTE1. 24, Created)

01-JUN-2003 (TYEMBLTE1. 24, Last sequence update)

01-OCT-2003 (TYEMBLTE1. 25, Last annotation update)

COST-2003 (TYEMBLTE1. 25, Last annotation update)

COST-2003 (TYEMBLTE1. 25, Last annotation update)

COST-146-PB

Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neophera; Endopterygota, Diptera; Brachycera; Muscomorpha;

NCBI_TAXID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.2%; Score 54; DB 5; Length 648; 69.2%; Pred. No. 9.2; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 648 AA; 69419 MW; 3F16E0EBF4B94CF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          701 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 69..
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGEGYQSRVDHPH 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 CCKGYVSRKDHGH 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
[2]
SEQUENCE FROM N.A.
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Melson D.R., Nelson K.A., Naxon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Poulard J., Puri V., Rese M.G.,
Reinert K., Remington K., Sanders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodager T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao Q., Zhao G., Zhao G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,

Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,

Hradecky P., Bergman C.M., Berman B.P., Carlson J.W., Celniker S.E.,

Clamp M.E., Drysdale R.A., Emmert D., Frise E., de Grey A.D.N.J.,

Harris N.L., Kronmiller B., Marshall B., Millburn G.H., Richter J.,

Russo S., Searle S.M.J., Smith E., Shu S., Smutniak F.,

Whitfield B.J., Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J.,
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

Bovidae; Caprinae; Ovis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lewis S.E.; "Annotation of Drosophila melanogaster genome."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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Submitted (JAN-2003) to the EM
EMBL; AE003642; AAO41187 1; -.
InterPro; IPR003341; DUF139.
InterPro; IPR006210; EGF like.
InterPro; IPR006210; IEGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02363; C_triplex; 16.
Pfam; PF00008; EGF; 1.
SMART; SM0181; EGF; 15.
PROSITE; PS01186; EGF 2; 6.
SEQUENCE 701 AA; 75366 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98 CGKGYVSRKDHGH 110
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les 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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CHAIN
SEQUENCE
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EMBL; 249879; CAA90036.1; -
EMBL; 249870; CAA90036.1; -
EMBL; 249809; CAA90036.1; -
EMBL; 249809; CAA90036.1; -
EMBL; 249809; CABB.

GO; GO:0016021; F.Integral to membrane; IEA.

GO; GO:0019886; P:antigen presentation, exogenous antigen; IEA.

GO; GO:0019886; P:antigen processing, exogenous antigen; IEA.

GO; GO:0019886; P:antigen processing, exogenous antigen via M. .; IEA.

GO; GO:0019886; P:antigen processing, exogenous antigen via M. .; IEA.

TherPro; IPR003597; Ig.-1.

EMBL; EMF000405; IG.-1.

EMBL; EMF000405; MGC II beta; 1.

EMBL; EMF000405; MGC II beta; 1.

EMBL; EMF000405; IGC1; 1.

EMBL; EMF00407; IGC1; 1.

EMBL; EMBL; EMBL; IMER; 1.

EMBL; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDITES BEGOGOSS; PubMed=3934274;

MEDITES BEGOGOSS; MEG_II_beta; I.

MEDITES BEGOGOSS; MEG_II_beta; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          031270 PRELIMINARY; PRT; 245 AA.
031270;
031270;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
Rat MHC RT1 class II B-beta chain (Fragment).
Rattus norvegicus (Rat).
Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NBEL TAXID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35.9%; Score 52; DB 7; Length 217; ilarity 52.9%; Pred. No. 6.1; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 AA; 24707 MW; 1E246E7DBC2AC6B2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 AA; 28069 MW; 6B21DADB2A4A299D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
Glycoprotein, MHC II, Transmembrane.
NON TER
SEQUENCE 245 AA; 28069 MW; 6B2ID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 GEVYTCLVDHPSLPSPV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GEGYQSRVDHPHFPKPI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunogenetics 49:735-737(1999).

REMBL; AF084932; AAD39082.1; -.
REMBL; AF084932; AAD39082.1; -.
REMBL; AF084932; AAD39082.1; -.
REMBL; AF084932; AAD39082.1; -.
REMBL; AF0840312; AAD39082.1; -.
REGO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0019884; P:antigen precentation, exogenous antigen; IEA.
GO; GO:0019884; P:antigen processing, exogenous antigen; IEA.
GO; GO:0019884; P:antigen processing, exogenous antigen via M. ..;
GO; GO:0009955; P:immune response; IEA.
REGO; GO:0006955; P:immune response; IEA.
RILEAFPO; IPR007110; Ig-like.
RILEAFPO; IPR003006; Ig-MHC.
RILEAFPO; IPR000353; MHC_II_beta.
REGO; PORO035; MHC_II_beta; 1.
REGO; PORO035; MHC_II_beta; 1.
REGO; PORO037; GO; II_Deta; 1.
REGO; PORO047; IGC; II_Deta; 1.
REGO; PORO047; IGC; II_Deta; 1.
REGO; PORO047; IGC; II_Deta; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ACI;
MEDLINE=99299366; PubMed=10369938;
Tian L., Wang M., Yu J., Kahan B.D., Stepkowski S.M.;
Tian Le, Wang M. tu J., Kahan B.D., Stepkowski S.M.;
Wholeotide sequences of three distinct complementary DNA clones
encoding rat class II major histocompatibility complex RTI.D beta-
chain proteins.";
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O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Class II MHC RTI.D(u) beta chain precursor.
Rattus norvegicus (Rat).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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CLASS II MHC RTI.D(A) BETA CHAIN.
48E220A69B374B3D CRC64;
Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.2%; Score 51; DB 7; Length 261;
47.1%; Pred. No. 10;
tive 3; Mismatches 6; Indels
                                                    6; Indels
                                                                                                                                                                                                                                                                                                            Q9TQA7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Class II MHC RTI.D(a) beta chain precursor.
  DB 7;
9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG'LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
Glycoprotein; MHC II; Signal; Transmembrane.
26 SIGNAL
                                                                                                                                                                                                                                                                                        261 AA
                                                       Mismatches
  Score 51;
Pred. No.
                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
  35.2%; Soc
Best Local Similarity 47.1%; Pre
Matches 8; Conservative 3;
                                                                                                                                                      176 GEVYTCQVEHPSLPSPV 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 GEVYTCQVEHPSLPSPV 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261 AA; 29496 MW;
                                                                                                      2 GEGYQSRVDHPHFPKPI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GEGYQSRVDHPHFPKPI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 47.1 nes 8; Conservative
                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat)
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2 GEGYQSRVDHPHFPKPI 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG LIKE; 1. PROSITE; PS00290; IG MHC; 1.
             34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
       Query Match
Best Local Similarity 36.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
tes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Q9ESH2;
                                                                                                                                                                                                                                                                                                              095536;
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                                                                                                                                                                                                                                                                                                                                                    GO, GO:0016021; C:integral to membrane; IEA.
GO; GO:0046012; F:MFC class II receptor activity; IEA.
GO; GO:0045012; F:MFC class II receptor activity; IEA.
GO; GO:001986; P:antigen processing, exogenous antigen; IEA.
GO; GO:001986; P:antigen processing, exogenous antigen via M. .; IEA.
GO; GO:006955; P:immune response; IEA.
InterPro; IPR00310; Ig_like.
InterPro; IPR003507; Ig_cl.
InterPro; IPR003507; Ig_cl.
InterPro; IPR0047; ig; I. beta.
PFGm; PF00047; ig; I. beta.
Probom; PR000328; MHC_II_beta; I.
Probom; PR000328; MHC_II_beta; I.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bovine viral diarrhea virus strain 4998/89.
Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
Pestivirus.
                                                                                                                            MEDLINE=99299366; PubMed=10369938;
Tian L., Wang M., Yu J., Kahan B.D., Stepkowski S.M.;
"Nucleotide sequences of three distinct complementary DNA clones
encoding rat class II major histocompatibility complex RTI.D beta-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Prevalence of genotypes 1 and 2 of bovine viral diarrhea virus in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
CLASS II MHC RT1.D(U) BETA CHAIN.
; 3C88B533514F531F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
35.2%; Score 51; DB 7; Length 264;
Best Local Similarity 47.1%; Pred. No. 11;
Matches 8; Conservative 3; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=4998/89;
Greiser-Wilke I.M.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lower Saxony, Germany.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ302959; CAC24757.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 140 140 140 1428D06B74391F74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UNN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS00290; IG MHC; 1.
Glycoprotein; MHC II; Signal; Transmembrane.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 AA.
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                                                                                                                                                                                                                                                       Immunogenetics 49:735-737(1999).
EMBL, AP084934; AAD39084.1; -.
PIR, A60497; A60497.
HSSP; P13760; 2SEB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             264 AA; 30138 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GEGYQSRVDHPHFPKPI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   glycoprotein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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STRAIN=4998/89;
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                                                                                                                                                                                                                                    chain proteins."
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SEQUENCE
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NON TER
SEQUENCE
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C199A59
DO 099A59
AC 099A59
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DT 01-JU
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Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Muzinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein J.;
"Multiplication of Mhc-DRB5 loci in the orangutan: implications for the evolution of DRB haplotypes.";
Mamm. Genome 4:159-170 (1993).
EMBL; S56369; AAD13881.1; -.
HSSP; P13758; 1AQD.
InterPro; IPR007101.1; -.
InterPro; IPR003107; Ig.cl.
InterPro; IPR003006; Ig_MHC.
Pfan; PR00047; ig. 1.
START; SM00407; ig. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pongo pygmaeus (Orangutan).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Laser M., Li Y., Xu L., Darden A., Wu B.X., Hazard E.S. III,
Crosson C., Ma J.X.;
"Identification and characterization of a novel gene induced by
ischemic preconditioning in the retina.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, ART15224, ARG09182.1;
InterPro; IPR007135; Autophagy. C.
InterPro; IPR007134; Autophagy. C.
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Score 50, DB 12, Length 140;
Pred. No. 7.9;
4; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE 142 AA; 15525 MW; 02C2C3AED44D063D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-WAR-2001 (TrEMBLrel. 16, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Preconditioning-inducible gene 1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.5%; Score 50; DB 7; 47.1%; Pred. No. 8;
                                                                                                                                                                                                                                                                                                                               142 AA
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                                                                                                                                                         69 CGHNFRKKEDLPHYP-----IGKC 87
                                                                                                                       1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Popy-DRB5*0603 protein (Fragment).
POPY-DRB5*0603.
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Pfam; PF03987; Autophagy_C; 1.
Pfam; PF03986; Autophagy_N; 1.
SEQUENCE 314 AA; 35838 MW; 4C64B70F7E909BDF CRC64;
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0; Gaps 0; Query Match
34.5%; Score 50; DB 11; Length 314;
Best Local Similarity 43.8%; Pred. No. 18;
Matches 7; Conservative 4; Mismatches 5; Indels

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Search completed: February 26, 2004, 08:27:17 Job time : 34.4 secs

us-09-701-623c-7.rag

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                    Copyright
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- protein search, using sw model OM protein February 26, 2004, 08:16:50; Search time 46.6 Seconds (without alignments) 151.581 Million cell updates/sec Run on:

US-09-701-623C-7

145 1 CGEGYQSRVDHPHFPKPIVRSITKC 25 score: Perfect so Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched: Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2003as:* geneseqp2003bs:* A Geneseq 29Jan04: geneseqp2001s:* geneseqp2002s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004a:*

## SUMMARIES

Description	Aay80000 Optimised	Abq74776 Rat IqE C	Rat	3 Rat	Aab06206 Immunogen		Abp96589 Rat IgE h	IgE (		٦		σ	ო		_		Aay80084 IgE immun	N		m	<b>T</b> #	<u>ــ</u>	Aay91215 Modified	Aay91217 Modified	Aay80014 IgE immun
QI	AAY80000	ABG74776	AAY79996	AAB03643	AAB06206	ABG74785	ABP96589	AAY80018	AAY80017	AAY80001	AAY79999	AAY80019	AAY80083	AAY80020	AAY80081	AAY80080	AAY80084	AAY68602	AAY91212	AAY79998	AAY68604	AAY91216	AAY91215	AAY91217	AAY80014
DB	<u>س</u>	ø	ო	ო	m	9	9	ო	ო	ო	m	m	ო	ო	ന	m	m	m	m	m	m	m	ო	ო	m
Length	25	114	313	340	341	346	428		46		25	45	45	46	57	62	63	25	25	~	4	4	42	42	42
% Query Match	100.0	84.1	84.1	84.1	84.1	84.1	84.1	83.4	83.4	73.1	72.4	72.4	72.4	72.4	72.4	72.4	72.4	71.0	71.0	71.0	71.0	71.0	71.0	71.0	71.0
Score	145	122	122	122	122	122	122	121	121	106	105	105	105	105	105	105	105	103	103	103	103	103	103	103	103
Result No.	F-1	7	ო	4	υ.	9	7	<b>α</b> ο	ማ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

		Aay91214 Modified Aay80011 IGE immun Aay80016 IGE immun Aay80010 IGE immun	S IGE Fept	Aay80002 IgE-GH3 d Aay80012 IGE immun Aau80298 Murine Ig Aau80299 Murine Ig Aau80297 Mouse IgE
ADD89950 AAY68605 AAY91218	AAY80007 ADD89951 AAY68603 AAY91213	AAY91214 AAY80011 AAY80016 AAY80010	AAY80013 AAY80015 AAY68606 AAY91219	AAY80008 AAY80012 AAU80298 AAU80299 AAU80297
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			103 71.0 103 71.0 103 71.0 103 71.0	
26 27 28 28 28	29 33 32 32	ሠ ພ ພ ພ ພ 4 ጥ ብ	E E E E E E E E E E E E E E E E E E E	14444 10644 1084

## ALIGNMENTS

Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylaxis; dermatitis. Optimised IgE-CH3 domain antigen peptide for rat IgE. AAY80000 standard; peptide; 25 AA. (first entry) 15-MAY-2000 AAY80000; AAY80000 ID AAY8 RESULT 1 

Rattus sp. Synthetic.

99WO-US013959. 21-JUN-1999; WO9967293-A1 29-DEC-1999.

(UNBI-) UNITED BIOMEDICAL INC. 98US-00100287. 20-JUN-1998;

Walfield AM; Wang CY,

WPI; 2000-160578/14.

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.

Claim 1; Page 99; 155pp; English.

The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, or containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermattisis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope

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This invention describes a novel antigenic peptide comprising amino acid residues of an IGE CH3 domain from a first species (ADE1) and amino acid residues of an IGE CH3 domain of a second unrelated species (ADE2), where ADE1 is conserved in the IGE CH3 domain of the second species and ADE2 is not conserved in the IGE CH3 domain of the first species. The novel antigenic peptide induces a non-anaphylacidistic peptide induces a non-anaphylacidistic sequence an animal. The invention also discloses the polymucleotide sequence an animal. The invention also discloses the polymucleotide sequence carcier, where the fusion protein antigenic peptide of the invention and a heterologous protein comprising the antigenic peptide and an antigenic fusion protein induces an anti-IGE immune response the invention have dermatological, antihilammatory and ophthalmological activity. The antigenic peptide described is capable of products of the invention have dermatological, antihilammatory and ophthalmological activity. The antigenic peptide described is capable of preventing IGE from binding to high affinity receptors on mast cells and basophils. The products of the invention are useful in the manufacture of a medicament for treating or preventing IGE-mediated allergic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated antigenic peptide comprising amino acid residues of CH3 domain of IgE molecule from first species and a second unrelated species, induces non-anaphylactic anti-IgE immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CH3 domain; IgB; antigen; non-anaphylactic; anti-IgB; fusion protein; dermatordical; antinflammatory; ophthalmological; allergy, asthma; allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilla; conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis;
(functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AA779994 to AA780084 represent amino acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 145; DB 3; Length 25; 100.0%; Pred. No. 1.6e-14; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGEGYQSRVDHPHFPKPIVRSITKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 31; 50pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Conservative
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N-PSDB; ACA55174.
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                                                                                                                                                                                                                                                                                   Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP1262491-A2.
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ID ABG74776

ID ABG74776

ABG77

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including asthma, allergic rhinitis, gastrointestinal allergies such as food allergies, eoshnophilia, conjunctivitis, glomerular nephritis, flea allergies or atopic dermatitis, in an animal, e.g. human or dog. The polynucleotide products are useful for treating igE-mediated allergic disorders, by gene therapy. Antigenic peptides comprising conserved amino acid residues of the CH3 domain of an IgE molecule from one species molecule from one species molecule from a second unrelated species are capable of inducing a high titre of anti-IgE anticolaise when administered to an animal without causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences in designing the constructs described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                         ·:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the spailon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell pitcope (functional in generically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulin lattory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-antantiantian anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                 Length 114;
                                                                                                                                                                                                                                                                                                 84.1%; Score 122; DB 6; Length 11 95.7%; Pred. No. 2.4e-10; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rat immunoglobulin E epsilon heavy chain SEQ ID NO:3.
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                                                                                                                                                                                                                                                                                                                                                                                                             84 GEGYQCRVDHPHFPKPIVRSITK 106
                                                                                                                                                                                                                                                                                                                                                                                 2 GEGYOSRVDHPHFPKPIVRSITK 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY79996 standard; protein; 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BIOMEDICAL INC.
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                                                                                                                                                                                                                                                                                                                                         22; Conservative
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                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                               Sequence 114 AA;
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                                                                                                                                                                                                                         invention
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                                                                                                                                                                                                                                                                                                     Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                         Matches
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(revised)
(first entry)

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The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgB and the heavy chain constant region 3 from the rat. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                          Immunogenic peptide consisting of opossum CH2, rat CH3 and opossum CH4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin \mathbb E in mammals.
                                                                                                                                                   Rat; opossum; immunoglobulin E; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide.
                  AAB06206 standard; protein; 341 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 2; 50pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            (RESI-) RESISTENTIA PHARM AB.
                                                                                                                                                                                                      Didelphis virginiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-365342/31.
                                                                                                                                                                                                                                                                   WO200025722-A2
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                                                                            12-SEP-2003
22-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Hellman LT:
                                                                                                                                                                                                                      Rattus sp.
Chimeric.
                                                 AAB06206;
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    AAB06206
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constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                           Rat; immunoglobulin E; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunogenic polypeptides useful for preventing the harmful effects immunoglobulin \boldsymbol{E} in mammals.
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                                                                                                           84.1%; Score 122; DB 3; Length 313; 95.7%; Pred. No. 7.2e-10; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               humans, against bacterial and viral infections and asthma, fur, pollen and food allergies and eczema
                                                                                                                                                                                                                                                                                                                                                                             Rat IgE heavy chain constant regions 2, 3 and 4.
                                                                                                                                                                                            GEGYQCRVDHPHFPKPIVRSITK 212
                                                                                                                                                                        GEGYOSRVDHPHFPKPIVRSITK 24
                                                                                                                                                                                                                                                                                  AAB03643 standard; protein; 340 AA.
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Best Local Similarity 95.7
Matches 22; Conservative
                                                                                                                          1 Similarity 95.7
22; Conservative
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                                                                             Sequence 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus sp.
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                                                                                                           Query Match
Best Local S
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99WO-SE001896 98US-0106652P. 99US-00401636.

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                                                                    Gaps
                                                                    ò
                                  Length 341;
                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                         Human CH2-rat CH3-human CH4 IgE-5 fusion protein.
                                Score 122; DB 3;
Pred. No. 7.9e-10;
0; Mismatches 1;
                                                                                                                            206 GEGYQCRVDHPHFPKPIVRSITK 228
                                                                                                   2 GEGYOSRVDHPHFPKPIVRSITK 24
                                                                                                                                                                                                                       ABG74785 standard; protein; 346 AA
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                                84.1%;
ilarity 95.7%;
Conservative 0
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                                Query Match
Best Local Similarity
Matches 22; Conserva
Sequence 341 AA;
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Gaps

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GEGYQCRVDHPHFPKPIVRSITK 217

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GEGYQSRVDHPHFPKPIVRSITK 24

antiallergic; antiaghmatic; immunosuppressive; vasotropic; cytostatic; dermatological; antiinflammatory; IgS-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhinitis; allergic asthmatatopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;

Immunoglobulin E, vaccine, IGE, cytotoxic T lymphocyte response; immune response; major histocompatibility complex; MHC; immunoge

Rat IgE heavy chain amino acid sequence SEQ ID NO:34.

immunogenic;

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This invention describes a novel antigenic peptide comprising amino acid residues of an IgE CH3 domain from a first species (ADE1) and amino acid residues of an IgE CH3 domain of a second unrelated species (ADE2), where DEE1 is conserved in the IgE CH3 domain of the first species. The novel antigenic peptide induces a non-anaphylactic antifgE immune response in an animal. The invention also discloses the polynucleotide sequence an animal. The invention also discloses the polynucleotide sequence arrier, where the fusion protein induces an anti-IgE immune response that does not cause anaphylaxis when administered to an animal. The products of the invention nave dermatological, antifilammatory and products of the invention have dermatological, antifilammatory and basophils. The products of the invention are useful in the manufacture of medicament for treating to preventing IgE from binding to high affinity receptors on mast cells and basophils. The products of the invention are useful in the manufacture of medicament for treating to preventing IgE-mediated allergies such as food allergies, ecsinophilia, conjunctivitis, glomerular nephritis, flea allergies, ecsinophilia, conjunctivitis, glomerular nephritis, flea clistoders, by gene therapy. Antigenic peptides comprising conserved amino acid residues of the CH3 domain of an IgE molecule from a second unrelated species are capable of inducing a high that a particular residues of the CH3 domain of an IgE molecule from a second unrelated species are capable of inducing a high residue of antimal residues of the capable of inducting a high relation of an immulative of anti-IgE antibodies when administered to an animal a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated antigenic peptide comprising amino acid residues of CH3 domain of IgE molecule from first species and a second unrelated species, induces non-anaphylactic anti-IgE immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences used in designing the constructs described in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.1%; Score 122; DB 6; Length 346; 95.7%; Pred. No. 8e-10; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                      22-MAY-2002; 2002EP-00253606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-MAY-2001; 2001US-0292638P
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Best Local Similarity 95.7
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown TM, Morsey MA;
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Homo sapiens.
                                                                                                                                                  EP1262491-A2.
                                                                                                                                                                                                                                                            04-DEC-2002.
                                               Rattus sp.
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Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I

Example 7; Page 167-169; 187pp; English.

protein.

Chen Z;

Yang Y, Barankiewicz T,

Chen SA,

WPI; 2003-268242/26.

08-AUG-2002; 2002WO-US026986. 13-AUG-2001; 2001US-0312120P. (IGET-) IGE THERAPEUTICS INC.

Rattus norvegicus. urticaria hives.

WO2003015716-A2.

27-FEB-2003

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The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E [19E], comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to naturally processed and presented 19Es peptides, where a peptide that induces such a response is identified. Also described are compositions:

(C1) comprising at least one immunogenic peptide (I) identified by (M1);

(C2) comprising at least one immunogenic peptide (I) identified by (M1);

(C2) comprising at least one immunogenic peptide (I) identified by (M1);

(C3) comprising at least one immunogenic peptide (I) identified by (M1);

(C3) comprising at least one intune geals that recognise at least one (I).

Where C1-3 are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented 19E peptides. C1-3 have antiallergic, antiasthmatic, immunosuppressive, vasotropic, dermatological, antialfammatory and cytostatic activities, and can be used as inducers of a CTL response against 19E, and in a vaccines. C1-3 can be used for modulating an IgE-mediated condition in a mammal at curse and the modulating an IgE-mediated condition in a mammal and the condition and a person of the mammal c1-3 that modulating an IgE-mediated condition as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IgE-mediated atopic hypersensitivity condition, IgE-mediated non-atopic hypersensitivity condition, IgE mediated non-atopic hypersensitivity condition, IgE myeloma in a mammal. Preferably, Cl-3 are useful for tracting atopic hypersensitivity conditions (such as allergic rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-atopic hypersensitivity conditions (such as anaphylaxis, and urticaria hives). The present sequence represents an IgE heavy chain amino acid sequence, which is given in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 GEGYQCRVDHPHFPKPIVRSITK 305
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es 22; Conserv
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ID AAY8
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Gaps

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ABP96589 standard; protein; 428 AA.

28-MAY-2003 (first entry)

ABP96589;

ABP96589
ID ABP9
XX
AC ABP9
XX
DT 28-1

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Sequence 46 AA;
                                     Unidentified
                                                               WO9967293-A1
                                                                                                                21-JUN-1999;
                                                                                                                                         20-JUN-1998;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes immunoglobulin E (IgE)-CH3 domain antiganic peptides (I). (I) have anti-allergic, anti-anaphylactic and antiganic peptides (I). (I) have anti-allergic, anti-anaphylactic and antiganic perpeties. (I) induces polyclonal antibodies specific of a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and bascphils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatities. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY9994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                       Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobenic; immunosfimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy; disease; immunisation; anti-allergic; anti-anaphylactic; anti-achmatic; asthma; anaphylaxis; dermatitis.
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immunogenic; immunostimulatory; carrier protein; helper T cell epitope;
                                                                                                                                                                                                                                                                                                                                            New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
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                                                IgE immunogenic peptide conjugate SEQ ID NO:25.
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                                                                                                                                                                                                                                                                                                                                                                                Claim 14; Page 76; 155pp; English.
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                                                                                                                                                                                                                                                                  (UNBI-) UNITED BIOMEDICAL INC
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Matches 22; Conservative
                        (first entry)
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                                                                                                                                                                                                                                                                                          Walfield AM;
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                        15-MAY-2000
                                                                                                                                       Unidentified
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AAY80018;
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antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic and antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic and antigenic peptides (1) induces polyclonal antibodies specific for a target effector afte on the epsilon-heavy chain of 1gB, and so a target effector afte on the epsilon-heavy chain of 1gB, and so containing triggering and activation of mast cells and basophils and downrequiation of 1gB synthesis. Conjugates, or fusion peptides, containing (1) are used for active immunication against 1gB-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatritis. Nucleic acids that encode these compounds are useful for combinant production of corresponding peptides or in DNA vaccines. Conjugates of (1) that include a promiscuous T helper cell epitope (1) that include a promiscuous T helper cell epitope (1) that include a promiscuous T helper cell epitope (1) trace and inverse subjects), in addition to a B cell carget epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maphylactogenic) antibodies. AAY9994 to AAY80084 represent amino acid sneaphylactogenic) antibodies. AAY9994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention
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antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
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88.0%; Pred. No. 1.2e-10;
ive 0; Mismatches 3; Indels
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Best Local Similarity 88.0
Matches 22; Conservative
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The present invention describes immunoglobulin E (IgE)-CH3 domain

antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and

antigenic properties. (I) induces polyclonal antibodies specific

at anti-estimatic properties. (I) induces polyclonal antibodies specific for

a target effector site on the epsilon-heavy chain of IgE, and so

c at arget effector site on the epsilon-heavy chain of IgE, and so

containing triggering and activation of mast cells and basophils and

containing (I) are used for active immunisation against IgE-mediated

containing (I) are used for active immunisation against IgE-mediated

containing (I) are used for active immunisation against IgE-mediated

containing production of corresponding peptides or in DNA vaccines.

correcombinant production of corresponding peptides or in DNA vaccines.

Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell

c target epitope, have increased immunogenicity and may include cyclic

constraints (disulfide bridge) to stabilise conformational features and

constraints (alsulfide bridge) to stabilise conformational features and

c maximize cross-reactivity to the natural target. They induce safe (non-

c anaphylactogenic) antibodies. AAY19094 to AAY80084 represent amino acid

constraints (non-measure and the present invention
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                                                                                                           antigenic peptide from the CH3 domain of immunoglobulin E, fusions immunization against allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.4%; Score 105; DB 3; Length 25
76.0%; Pred. No. 1.6e-08;
.ive 0; Mismatches 6; Indels
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                                                                                                                                                                                             Claim 1; Page 99; 155pp; English
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Best Local Similarity 76.0
Matches 19; Conservative
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                     Walfield AM;
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                                                                 WPI; 2000-160578/14.
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                       Wang CY,
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                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes immunoglobulin E (IGE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic properties. (I) induces polyclonal antibodies specific (a target effector site on the epsilon-heavy chain of IGE, and so preventing triggering and activation of mast cells and basophils and downward (I) are used for active immunisation against IGE-mediated allergies, e.g. food allergies, sorbma, anaphylaxis, or flea-allergy dermaities. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell politope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maphylactogenic) antibodies. APY 9994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                           New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
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Best Local Similarity 80.0
Matches 20, Conservative
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                                           The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic antigenic peptides (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatities. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epicope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maphylaxing cross-reactivity to the natural target. They induce safe (nonanaphylaxing) antibodies. AAY19994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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Pred. No. 3e-08;
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     14; Page 76; 155pp; English
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Best Local Similarity
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antisedimatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and contenting triggering and activation of mast cells and basophils and containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
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containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy defermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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Best Local Similarity
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antigenic peptides (I). Induces polyclonal antibodies specific anti-aschmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of 19E, and so containing triggering and activation of mast cells and bacophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (nonamphylactogenic) antibodies. AAV19994 to AAV80084 represent amino acid anaphylactogenic) antibodies. AAV19994 to AAV80084 represent amino acid
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maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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72.4%; Score 105; DB 3; Length 46;
Best Local Similarity 76.0%; Pred. No. 3.1e-08;
Matches 19; Conservative 0; Mismatches 6; Indels
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72.4%; Score 105; DB 3; Length 57; 76.0%; Pred. No. 3.9e-08;

Query Match Best Local Similarity

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6; Indels
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Job time: 46.6 secs
                            1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                            33 CGETYYSRVTHPHLPKDIVRSIAKC 57
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RESULT 15
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APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REPERENCE: P-1047
CURRENT APPLICATION NUMBER: US/10/409, 772
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: US/09/479,614
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 29
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Publication No. US20030096369A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgE vaccines
FILE REFERENCE: PC11011A
CURRENT APPLICATION NUMBER: US/10/152,190
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1: 14
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US-10-409-772-29
IS-10-409-772-29
Publication US/10409772
Publication No. US/030216565A1
GENERAL INFORMATION:
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ORGANISM: Dog CH3 domain
US-10-152-190-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Felis catus
US-10-409-772-29
; ORGANISM: Felis catus
US-10-409-772-2
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RESULT 14 US-10-152-190-3 Sequence 3, Application US/10152190 ; Publication No. US20030096369A1

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Publication No. US20030096369A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgE vaccines
FILE REFERENCE: PCIIOLIA
CURRENT APPLICATION NUMBER: US/10/152,190
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 28
SOFTWARR: Patentin Ver. 2.1
SEQ ID NO 2
IENGTH: 117
GENERAL INFORMATION:

APPLICANT: Morsey, Mohamad A.

TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgE vaccines
FILE REPERENCE: PCIIOLIAA

CURRENT APPLICATION NUMBER: US/10/152,190

CURRENT FILING DATE: 2002-05-21

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO
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60.7%; Score 82; DB 14;
Best Local Similarity 65.2%; Pred. No. 0.00011;
Matches 15; Conservative 4; Mismatches 4.
                                                                                                                                                                                                                                            LENGTH: 115
TYPE: PRT
ORGANISM: Human CH3/dog CH3 domain chimera
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ORGANISM: Human CH3/dog CH3 domain fusion
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TYPE: PRT
ORGANISM: Felis catus
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US-10-214-524-25
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Matches
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VS-10-409-77
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Sequence 2, Application US/09479614

Publication No. US20030013183A1

Publication No. US20030013183A1

Sequence 2, Application US/09479614

Publication No. US20030013183A1

APPLICANT: Weber, Eric

TITLE OF INVENTION: Faline Immunoglobulin E Molecules and Related Methods

FILE REFERENCE: P-1047

CURRENT FILING DATE: 1090-01-07

EARLIER FILING DATE: 1999-01-07

NUMBER OF SEQ ID NOS: 34

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 2
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                                            294 GETYQCKVTHPDLPKDIVRSIAK 316
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2 GETYKSTVSHPDLPREVVRSIAK 24
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Publication No. US20030013183A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
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ORGANISM: Felis catus
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RESULT 11
US-10-409-772-2
is Sequence 2, Application US/10409772
is Publication No. US20030216565A1
is GENERAL INFORMATION:
is APPLICANT: McCall, Catherine
is APPLICANT: Weber, Exic
it TILE OF INVENTION: Peline Immunoglobulin E Molecules and Related Methods
it TILE OF INVENTION: Peline Immunoglobulin E Molecules and Related Methods
is TILE APPLICATION NUMBER: US/10/409,772
is CURRENT FILING DATE: 2003-04-07
is PRIOR APPLICATION NUMBER: US/09/479,614
is PRIOR FILING DATE: 2000-01-07
is NUMBER OF SEQ ID NOS: 34
is SOFTWARE: Patentin Ver. 2.0
is SEQ ID NO 2
is LENGTH: 496
it TYPE: PRI
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US-10-214-524-5.

US-10-214-524-5.

Publication No. US20030073142A1

GENERAL INFORMATION:

APPLICANT: Chen, Swey-Shen Alex

APPLICANT: Yang, Yong-Min

APPLICANT: Yang, Yong-Min

APPLICANT: Chen, Zhong

TITLE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF

FILE REPREEDED 01012-1.1

CURRENT APPLICATION NUMBER: US/10/214,524

CURRENT FILING DATE: 2002-08-08

PRIOR FILING DATE: 2001-08-13

NUMBER OF SEQ ID NOS: 61

SEQ ID NO 25

IENGTH: 496

TYPE: PAT

TYPE: PAT

CORGANISM: Cat (Felis catus)

US-10-214-524-25
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TITLE OF INVENTION: Feline Immunoglobulin B Molecules and Related Methods FILE REFERENCE: P-1047
CURRENT APPLICATION NUMBER: US/09/479,614
CURRENT FILING DATE: 2000-01-07
EARLIER APPLICATION NUMBER: 60/115,033
EARLIER FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 34
SCOTTWARE: Patentin Ver. 2.0
SEQ ID NO 29
LENGTH: 496
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Best Local Similarity 69.6%; Pred. No. 1.8e-05;
Matches 16; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
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Query Match 69.6%; Score 94; DB 14; Length 45; Best Local Similarity 64.0%; Pred. No. 5.5e-07; Matches 16; Conservative 4; Mismatches 5; Indels
                                                                                              NAME/KEY: misc_feature

) LOCATION: (20)..(20)

) OTHER INFORMATION: Xaa indicates epsilon-Lys

US-10-076-674-11
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; LOCATION: (20)...(20)
; OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-1614-11
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, Sequence 11, Application US/10355161A
, Publication No. US20040009897A1
, GENERAL INFORMATION:
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Best Local Similarity
Matches 16; Conservat
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US-09-479-614-14
             ORGANISM: Human
FEATURE:
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Sequence 11, Application US/10076674

Publication No. US20330165478A1

GENERAL INFORMATION:
APPLICANT: SOKOll, Kenneth K.
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Patentin version 3.1

SQITWARE: Patentin version 3.1

TYPE: PRT
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Sequence 10, Application US/10355161A
Publication No. US2004009897A1
GENERAL INFORMATION:
APPLICANTON:
TITLE OF INVENTION: Stabilised Synthetic Immunogen Delivery System
TITLE OF INVENTION WIMBER: US/10/355,161A
CURRENT APPLICANTON NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR FILING DATE: 2002-02-14
TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System FILE REFERENCE: Immunogen Delivery System CURRENT APPLICATION NUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 44
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69.6%; Score 94; DB 15; Length 44;
Best Local Similarity 64.0%; Pred. No. 5.4e-07;
Matches 16; Conservative 4; Mismatches 5; Indels
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: LOCATION: (19)...(19)

: OTHER INFORMATION: Xaa indicates epsilon-Lys

US-10-355-161A-10
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i LOCATION: (19)..(19)
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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Sequence 14, Application US/09479614

Sequence 14, Application US/09479614

Publication No. US20030013183A1

GENERAL INFORMATION:
APPLICANT: McCall, Catherine
APPLICANT: Weber, Eric
TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
FILE REFERENCE: P-104710 NUMBER: US/09/479,614

CURRENT APPLICATION NUMBER: US/09/479,614

CURRENT FILING DATE: 1999-01-07

EARLIER PPLING DATE: 1999-01-07

SOFTWARE: Patentin Ver: 2.0

SEQ ID NO 14

LENGTH: 431
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                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sokoll, Kenneth K.
ITILE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
FILE REFERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT FILING DATE: 2003-01-31
PRIOR APPLICATION NUMBER: US 10/076674
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
LENGTH: 45
TYPE: PRT
ORGANISM: Human
CREANISM: Human
CREANISM: Human
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Sequence 11, Sequence 10,

sequence 12, Appl Sequence 11, Appl Sequence 28, Appl Sequence 33, Appl Sequence 26, Appl Sequence 26, Appl Sequence 4, Appli Sequence 6, Appli Sequence 10, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 27, Appli

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Sequence 30. Application US/10214524

Publication No. US20030073142A1

GENERAL INFORMATION:
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Chen, Zhong
ITILE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
FILE REPREMENT: Chen, Zhong
ITILE OF INVENTION: IMMUNOGLOBULIN E VACCINES AND METHODS OF USE THEREOF
FILE REPREMENT: Chen, Zhong
CURRENT APPLICATION NUMBER: US/10/214,524
CURRENT PILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/312,120
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SEQ ID NO 30
IENTHER SEG ENTER PATENTING THE SEG ENTER PATE
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              4 US-10-176-664-11

4 US-10-176-664-11

4 US-10-152-190-10

4 US-10-152-190-11

4 US-10-124-28

4 US-10-214-524-28

4 US-10-214-524-33

4 US-10-214-524-33

4 US-10-214-524-33

5 US-10-214-524-33

6 US-10-214-524-36

7 US-10-214-524-36

8 US-10-214-524-33

8 US-10-214-524-36

8 US-10-214-524-36

8 US-10-315-40

8 US-09-949-375A-6

8 US-09-949-375A-10

8 US-10-176-664-8

8 US-10-214-524-27
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Sequence 10, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
APPLICANT: Sokoll, Kenneth K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Horse (Equus caballus)
  US-10-214-524-30
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RESULT 2
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                                                                                                                                                February 26, 2004, 08:27:32; Search time 26.2 Seconds (without alignments) 201.482 Million cell updates/sec
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Seq
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCCMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCCMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCCMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCCMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCCMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCCMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCCMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCCMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCCMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCCMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCCMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCCMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCCMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-075-674-10
US-10-355-161A-10
US-10-355-161A-11
US-10-355-161A-11
US-09-479-614-14
US-09-479-614-2
US-09-479-614-2
US-09-479-614-2
US-09-479-614-2
US-10-10-409-772-2
US-10-409-772-2
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US-10-152-190-3
US-10-152-190-2
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135
1 CGETYKSTVSHPDLPREVVRSIAKC 25
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext
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Maximum DB seq length: 200000000
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Match
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                                                                                                                                                                                                                                                                                                                                               Scoring table:
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Gaps

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antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic and antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic and antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic and antiacture at the antibodies specific for a target effector site on the epsilon-heavy chain of 195, and so a target effector site on the epsilon of mast cells and basophils and downregulation of 195 synthesis. Conjugates, or fusion peptides, containing (1) are used for active immunisation against 195-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy certaities. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (1) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maphylactogenic) antibodies. Axy1994 to AAX80084 represent amino acid snaphylactogenic) antibodies. Axy1994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helper T cell epitope; peptide immunogen; LHRH;
luteinising hormone-releasing hormone; spermatogenesis; ovulation;
oseftrus; sexual development; sex hormone; promiscuous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
breast cancer; endometriosis; boar taint; meat quality; immunocastration.
                                                                                                                                                                                                                            New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                   present invention describes immunoglobulin E (IgE)-CH3 domain
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Pred. No. 1.3e-07;
4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide sequence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY68604 standard; peptide; 42 AA
                                                                                                                                                                                                                                                                               Claim 1, Page 21; 155pp; English.
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                                                                                                                    (UNBI-) UNITED BIOMEDICAL INC
                                                                                    98US-00100287.
                                                  99WO-US013959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69.6%;
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Best Local Similarity 64.09
                                                                                                                                                      Wang CY, Walfield AM;
                                                                                                                                                                                        WPI; 2000-160578/14.
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                                                                                   20-JUN-1998;
                                                  21-JUN-1999;
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                  29-DEC-1999.
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The specification describes peptide immunogens comprising a synthetic releasing hormone (IHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, cestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                             New peptide immunogen containing luteinizing hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 95; 102pp; English.
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                              Thr
                                                                                                                                                                                                                                                                                                                   (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                      99WO-US013960.
label= Gly,
                              label= His,
                                                                                          label= Ile,
                                                           label= Lys,
                                                                                                                        label= Gly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-160562/14.
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Best Local Similarity
               Misc-difference
                                                                            Misc-difference
                                                                                                         Misc-difference
                                             Misc-difference
                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                    21-JUN-1999;
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                                                                                                                                                                                                                      29-DEC-1999
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helper T cell (Th) epitope and a target antigen, luteinising hormone-releasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of a promise. Every sexual development and secretion of sex hormones. Frovision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum and thus high attibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometricosis); to prevent boar taint (and appears in the specification.
        8$66666666666588
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Sequence 25 AA;

Gaps .. 69.6%; Score 94; DB 3; Length 25; 64.0%; Pred. No. 1.3e-07; ive 4; Mismatches 5; Indels 1 CGETYKSTVSHPDLPREVVRSIAKC 25 1 CGETYQSRVTHPHLPRALMRSTTKC 25 Query Match
Best Local Similarity 64.0
Matches 16; Conservative d 8

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AAY91212;

AAY91212 standard, peptide, 25 AA

Modified human IgE CH3 domain, SEQ ID NO:92.

(first entry)

22-MAY-2000

Promiscuous T-cell epitope, meaales virus F protein; MVF, hepatitis B virus surface antigen, HBV, immunogenic; B-cell epitope, luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; OD receptor, HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin B; IgE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.

Homo sapiens Synthetic.

W09966957-A2

29-DEC-1999

99WO-US013975. 21-JUN-1999;

98US-00100412. 20-JUN-1998; (UNBI-) UNITED BIOMEDICAL INC

Wang CY;

WPI; 2000-160564/14.

New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis antigenic site, for immunization or human immune deficiency virus.

Example 6; Page 40; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The Th epitopes and peptide immunogens containing them, are used to induce a T helper cell response, specifically against Plasmodium falciparum, cholestery! ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunoreactive self-antigen or tumour antigen. The Th epitopes and 

communications (HIV) foot-and-mouth disease or malaria); for cancer infections (HIV) foot-and-mouth disease or malaria); for cancer communications (HIV) foot-and-mouth disease or malaria); for cancer infections (HIV) foot-and-mouth disease or malaria); for cancer communications (HIV) foot-and-mouth disease or malaria); for cancer cleasing hormone (HIRB) for contraception, treatment of hormone-cleasing hormone contracts are contracted inferences and management and management and managementally diverse subjects) into an immunogan improves capacity to conduct on of antibodies against a target antigen. The can replace carrier proteins and pathogen-derived Thelper epitopes. Sequence AAV91121 contracts and pathogen-derived Thelper epitopes sequence AAV91121 contracts and pathogen-derived Thelper epitopes sequence AAV91121 contracts and pathogen-derived Thelper epitopes sequence AAV91121 contracts and AAV91224 contracts and sequences AAV91142. Pathogen-derived from the HIV epitopes have not the NVF Thelpitope. Sequence AAV91143 represents a promiscuous Thelpitope from the map to peptides comprising an LHRH sequence joined to a promiscuous Thelpitope. AAV91167 is the LHRH target antigenic peptide comprising somatcostatin and a Thelpitope. AAV91201 are antigenic peptides comprising somatcostatin and and AAV91201 are antigenic peptides comprising somatcostatin and and peptides. AAV91201 are antigenic peptides comprising somatcostatin and and peptides. AAV91201 are antigenic peptides which may be used to prevent HIV infection of The Company of The Company of Thelpitope. AAV91220 is a peptide from the AV91221 v91225 comprise the Competence of a human 19E (immunogens end AAV91221 v91225 comprise the competide and a Thepitope. AAV91220 is a peptide ferived from the comprise the Competence of antigen and a Thepitope and and AAV91221 v91225 comprise the competide and and MVPT The peptide and and antigenic and and AAV91221 are HIV-1 neutralising a CTP-derived peptides and and AAV9128 - v91231 are antigenic peptides and and AAV9 

Seguence 25 AA;

ö 69.6%; Score 94; DB 3; Length 25; 64.0%; Pred. No. 1.3e-07; 1.ve 4; Mismatches 5; Indels Conservative Query Match Best Local Similarity

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Gaps

1 CGETYKSTVSHPDLPREVVRSIAKC 25 

AAY79998 standard; peptide; 25 AA.

RESULT 14

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15-MAY-2000 (first entry)

Optimised IgE-CH3 domain antigen peptide for human IgE.

Immunoglobulin B; IgB; epsilon heavy chain; antigenic; antigen; immunoglobulin Bingen; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis. 

Homo sapiens Synthetic.

WO9967293-A1

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Sequence 63 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified
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Matches
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                                                                                                                                                                 The present invention describes immunoglobulin B (IgB)-CH3 domain antiganic peptides (1). (1) have anti-allergic, anti-anaphylactic and antiganic peptides (1). (1) induces polyclonal antibodies specific or a target effector site on the epsilon-heavy chain of IgB, and so reventing triggering and activation of mast cells and basophils and downrequiation of IgB synthesis. Conjugates, or fusion peptides, containing (1) are used for active immunisation against IgB-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermattis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (1) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maphylactogenic) antibodies. AAY9994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                                                      New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IgE immunogenic peptide conjugate SEQ ID NO:91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                                                            Claim 14; Page 77; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY80084 standard; peptide; 63 AA
                        (UNBI-) UNITED BIOMEDICAL INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%;
72.0%;
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98US-00100287
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                                                  Walfield AM;
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Best Local Similarity
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                                                                             WPI; 2000-160578/14.
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 62 AA;
 20~UUV-1998;
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic properties. (I) induces polyclonal antibodies specific a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated alergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. Axy3994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention
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New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                77.8%; Score 105; DB 3; Length 63
72.0%; Pred. No. 7.2e-09; Pred. No. 7.2e-09; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 92; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide sequence of the invention.
                                                                          English.
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                                                                          14; Page 77; 155pp;
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us-09-701-623c-84.rag

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New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
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                                                                                                                                                                           (UNBI-) UNITED BIOMEDICAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57 AA;
Unidentified.
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                                   WO9967293-A1
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                                               Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogratic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; authmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                          antigenic peptide from the CH3 domain of immunoglobulin E, fusions immunization against allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IgE immunogenic peptide conjugate SEQ ID NO:88.
                IgE immunogenic peptide conjugate SEQ ID NO:27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY80081 standard; peptide; 57 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 77; 155pp; English
                                                                                                                                                                                                                                                                                                                   (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                               99WO-US013959.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                 20-JUN-1998;
                                                                                                                                       Unidentified
                                                                                                                                                                           NO9967293-A1
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The present invention describes immunoglobulin E (IGE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic properties. (I) induces polyclonal antibodies specific canti-asthmatic properties. (I) induces polyclonal antibodies specific cantiarget effector site on the epsilon-heavy chain of IGE, and so a target effector site on the epsilon-heavy chain of IGE, and so containing (I) are used for active immunisation against IGE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatties. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (I) that include a promiscuous T helper cell epitope (I) that include a promiscuous T helper cell epitope (I) that include a promiscuous T helper cell epitope (I) that include a promiscuous T helper cell epitope (I) that include a promiscuous T helper cell epitope (I) that include a promiscuous T helper cell epitope (I) that include a promiscuous C (I) that I) that I tha
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Claim 14; Page 77; 155pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US013959.
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epitope;

Immunoglobulin E; IgE; epsilon heavy chain, antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epit antibody; allergy; allergy disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

Unidentified 409967293-A1

IgE immunogenic peptide conjugate SEQ ID NO:90.

(first entry)

15-MAY-2000

AAY80083;

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AAY80083 standard; peptide; 45

RESULT 7

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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic peptides (I) induces polyclomal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergys (I) are used for active immunisation against IgE-mediated allergys allergies, e.g. food allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatities. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY9994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin B; IgB; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
                                                Gaps
                                              ..
  77.8%; Score 105; DB 3; Length 25; 72.0%; Pred. No. 2.4e-09; ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77.8%; Score 105; DB 3; Length 45; 72.0%; Pred. No. 4.8e-09; ive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                     immunogenic peptide conjugate SEQ ID NO:26.
                                                                                   1 CGETYKSTVSHPDLPREVVRSIAKC 25
                                                                                                           CGETYYSRVTHPHLPKDIVRSIAKC 25
                                                                                                                                                                                                                               AAY80019 standard; peptide; 45 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; Page 76; 155pp; English.
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                                                                                                                                                                                                                                                                                                              (first entry)
Query Match
Best Local Similarity 72.0
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
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New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.

(UNBI-) UNITED BIOMEDICAL INC.

Walfield AM;

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WPI; 2000-160578/14.

98US-00100287.

20-JUN-1998;

21-JUN-1999;

29-DEC-1999

Claim 14; Page 77; 155pp; English.

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The present invention describes immunoglobulin E (IgB)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgB, and so preventing triggering and activation of mast cells and basophils and downregulation of IgB synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgB-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermartitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. (Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      al target. They induce safe (non-
to AAY80084 represent amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      maximize cross-reactivity to the natural target. They induce so anaphylactogenic) antibodies. AAY79994 to AAY80084 represent an sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.8%; Score 105; DB 3;
ilarity 72.0%; Pred. No. 4.8e-09;
Conservative 4; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 CGETYYSRVTHPHLPKDIVRSIAKC
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Les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45 AA;
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ID AAY8
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AC AAY8
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DT 15-M
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Gaps

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Best Local Similarity 72.0 Matches 18; Conservative

Gaps

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Length 424;

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The present invention describes a method (MI) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E [192], comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to naturally processed and presented igE peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (MI); (C2) comprising at least one immunogenic peptide (I) identified by (MI); (C2) comprising antigen-presenting cells that recognise at least one (I). Where C1-3 are able to bind to at least one MHC class I molecule and to clicit in a mammal a CTL response to maturally processed and presented igE peptides. C1-3 have antiallered; antiasthmatic, immunosuppressive, vasotropic, dermatological, antiaflammatory and cytostatic activities, and can be used as inducers of a CTL response against IgE, and in vaccines. C1-3 are useful for modulating an IgE-mediated condition in mammal. C1-3 are useful for modulating an IgE-mediated condition in mammal. C1-3 are useful for modulating an igE-mediated condition as mammal. Enemalized atopic hypersensitivity condition, IgE mediated non-atopic hypersensitivity condition, IgE mediated atopic cuseful for treating atopic hypersensitivity conditions (such as allergic useful for treating atopic hypersensitivity conditions (such as allergic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin E, vaccine, IgE, cytotoxic T lymphocyte response, immune response, major histocompatibility complex, MHC; immunogenic, antiallergic, antiasthmatic, immunosupressive, vasotropic, cytostatic, dermatological; antiinflammatory; IgE-mediated condition; food allergy, atopic hypersensitivity condition, allergic rhinitis, allergic asthma, atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                      Score 112; DB 5; Length 42:
Pred. No. 5.7e-09;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Horse IgE heavy chain amino acid sequence SEQ ID NO:30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 157-160; 187pp; English.
                                                                                                                                                                 288 GETYKCTVSHPDLPREVVRSIAK 310
                                                                                                                                2 GETYKSTVSHPDLPREVVRSIAK 24
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                                                                                                                                                                                                                                                                                      ABP96585 standard, protein, 569
                                        83.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-AUG-2002; 2002WO-US026986.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-AUG-2001; 2001US-0312120P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (IGET-) IGE THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                             1 Similarity 95.7
22; Conservative
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Sequence 424 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equus caballus.
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                                   Query Match
Best Local (
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anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid
sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobenic; immunosfimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-
atopic hypersensitivity conditions (such as anaphylaxis, and urticaria
hives). The present sequence represents an IGE heavy chain amino acid
sequence, which is given in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
                                                                                                                                                                     Gaps
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                                                                                                                                 Length 569;
                                                                                                                               83.0%; Score 112; DB 6; Length 56
95.7%; Pred. No. 8.1e-09;
ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Optimised IgE-CH3 domain antigen peptide for dog IgE.
                                                                                                                                                                                                                                              433 GETYKCTVSHPDLPREVVRSIAK 455
                                                                                                                                                                                                           2 GETYKSTVSHPDLPREVVRSIAK 24
                                                                                                                                                                                                                                                                                                                                             AAY79999 standard; peptide; 25 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 99; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNBI-) UNITED BIOMEDICAL INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                 Query Match
Best Local Similarity 95.7
Matches 22; Conservative
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                                                                                            Sequence 569 AA;
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Synthetic.
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(functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies, AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence encoding part of an equine immunoglobulin G, useful for preparing isotype-specific antibodies for diagnosis and treatment of allergy in horses.
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                                                                                                                                                                                                                                                                                                                                                                                                             Equine IgE heavy chain constant region C-epsilon allotype A.
                                                                                                                                                                          0; Indels
                                                                                                                                            Length
                                                                                                                                       100.0%; Score 135; DB 3;
100.0%; Pred. No. 4.1e-14;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                          1 CGETYKSTVSHPDLPREVVRSIAKC 25
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/note= "CH2 domain"
206. .312
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/note= "CH1 domain"
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/note= "CH3 domain"
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/note= "CH4 domain"
                                                                                                                                                                                                      1 CGETYKSTVSHPDLPREVVRSIAKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-DEC-2001; 2001WO-DE004810
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                        25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-508803/54.
N-PSDB; ABL61246.
                                                                                                                                                        Similarity
                                                                                                            Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Equus caballus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200250280-A2
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                                                                                                                                       Query Match
Best Local 6
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sequence represents a fragment of the equine IgE heavy chain constant region C-epsilon allotype a (Cea), used in the method of the invention for IgE-isotype recombinant immunoglobulin production
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA sequence encoding part of an equine immunoglobulin G, useful for preparing isotype-specific antibodies for diagnosis and treatment of allergy in horses.
                                                                                                                                                                                                                                                                                                                                                                                   Ceb; equine; horse; heavy chain; constant region; allotype b; IgE; C-epsilon b; immunoglobulin E; antiallergic; allergy.
                                                                                                                       ö
                                                                                        Length 424;
                                                                                                                                                                                                                                                                                                                                                     Equine IgE heavy chain constant region C-epsilon allotype
                                                                                                                      1; Indels
                                                                                       83.0%; Score 112; DB 5;
95.7%; Pred. No. 5.7e-09;
live 0; Mismatches 1;
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                                                                                                                                                                                 288 GETYKCTVSHPDLPREVVRSIAK 310
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'note= "CH1 domain"
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/note= "CH4 domain"
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                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .312
                                                                                                       Local Similarity 95.7 es 22; Conservative
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                                                              Sequence 424 AA;
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allergy in
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Best Local S:
Matches 22
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Aamsollo4 Equine Ig
Abp96585 Horse Ige
Aay79999 Optimised
Aay80019 IgE immun
Aay80020 IgE immun
Aay80080 IgE immun
Aay801215 Modified s
Aay91215 Modified s
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Aay91219 Modified Aay80007 IgE peptide S
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Aay8000 IgE Peptide S
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                                                                                                                                                                                                                           1586107
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 CGETYKSTVSHPDLPREVVRSIAKC 25
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Maximum Match 100%
Listing first 45 summaries
                                              OM protein - protein search, using sw model
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Aay91213 Modified Aay901214 Modified Aay80011 1GE immun Aay80010 1GE immun Aay80010 1GE immun Aay80012 1GE immun Aay80012 1GE immun Aay80012 1GE immun Aay96060 Peptide S Aay91219 Inv epito Aay80012 1GE immun Abp96580 Cat 1GE h Abu09338 Feline 1G Aay80018 1GE immun Aay80010 1GE immun Aay80017 1GE immun Aay80017 1GE immun Aay80017 1GE immun Aay80017 1GE immun	de for horse IgE. hain; antigenic; antigen; r protein; helper T cell epitope; r munisation; anti-allergic; hma; anaphylaxis; dermatitis.	Wang CY, Walfield AM; WPI; 2000-160578/14.  New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.  Claim I; Page 146; 155pp; English.  Claim I; Page 146; 155pp; English.  The present invention describes immunoglobulin E (1gE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic peptides (I). (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of 1gE, and so a target effector site on the epsilon-heavy chain of 1gE, and so downregulation of 1gE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against 1gE-mediated dermatities. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines.  Conjugates of (I) that include a promiscuous T helper cell epitope
AAY91213 AAY80011 AAY80016 AAY80016 AAY80015 AAY80015 AAY80015 AAY80012 AAY80012 AAY80010338 AAY80010338 AAY80010338 AAY80010338 AAY80010338 AAY80010338 AAY80010338 AAY80010338 AAY80010338 AAY80017 AAY80017 AAY80018 AAY80017 AAY80017 AAY80017 AAY80017	ALIGNWE 25 AA. 19en pepti on heavy c 77, carificatic, ast matic; ast	m the CH3 domain allergy.  English.  Cribes immunoglol cribes immunoglol the epsilon-head activation of machesis. Conjugator or active immunitate encode the corresponding political appropriation of corresponding political appropriation and active immunitation active
<b></b>	n n ar replace ( 13.99)	finst all states all s
44400000000000000000000000000000000000	irst entry) H3 domain ant E3 IgE; epsil munostimulato ic; anti-asth ic; anti-asth 99WO-US013959 99US-00100287	11eld AM; 578/14.  peptide from against in 146; 155pp; Twention dess tides (1) (C properties on iggering and nof iggering and nof iggering and nof grow alse in 16 on idgering and nof iggering and in in in that in
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Last sequence update)
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PRT;

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Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                           Strausberg N. S. Strausberg N. Strausberg N. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. InterPro; IPR0030110; Ig-1ike. InterPro; IPR00306; Ig-WC. Pfam; PF00047; ig; 5. Pfam; PF00047; ig; 5. PROSITE; PS001599; IG-IKE; 5. PROSITE; PS001599; IG-IKE; 5. PROSITE; PS001599; IG-IKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
SEQUENCE 588 AA, 64438 MW, FC60DBAD82B39FD7 CRC64;
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Job time : 35.4 secs
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442 GERFICTVTHIDLPSPLKQTISR 464
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  408 CSKTITKTVTGPDGRREVVKEV 429
                                                                                                         QBWUX4;
QBWUX4;
01-MAR-2002 (TrEMBLrel. 20, Cr
01-MAR-2003 (TrEMBLrel. 20, Le
01-OCT-2003 (TrEMBLrel. 25, Le
Hypothetical protein.
                                                                                            PRELIMINARY;
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TISSUE-Lymph;
                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                     RESULT 15
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TISSUE-Human rectum tumor;

TISSUE-Human rectum tumor;

Blocker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann to the EMBL/GenBank/DDBJ databases.

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, BX538077; CAD98001.1; -. Hypothetical protein.

Hypothetical protein.

SEQUENCE 492 AA; 53776 MW; IE7A15760F0CA74B CRC64;
                                                                                                                                                                                                                                                                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686C02218 (Fragment).
DKFZP686C02218.
Hymo sapiens (Human).
Bukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                       Query Match
37.8%; Score 51; DB 4; Length 478;
Best Local Similarity 39.1%; Pred. No. 32;
Matches 9; Conservative 5; Mismatches 9; Indels
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC005467; AAH05467.1; -.
HSSP; P02671; 1FZA.
MGD; MGI:1316726; Fga.
SEQUENCE 557 AA; 61325 MW; C47F496D1BA432DE CRC64;
    1 1
478 AA; 51620 MW; 4AFCB541F3217CA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TIEMBLrel. 17, Created)
01-JUN-2001 (TIEMBLrel. 17, Last sequence update)
01-OCT-2002 (TIEMBLrel. 22, Last annotation update)
Fibrinogen A alpha polypeptide.
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NON TER
SEQUENCE
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Q7Z374
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Gaps

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Best Local Similarity 39.1
Matches 9; Conservative
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Q7Z379
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EMBL; AR006138; AAK03079.1; -.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Human full-length cDNA clone CSODD006f102 of neuroblastoma of Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                Pasteurella multocida.
Bacteria, Proteobacteria, Gammaproteobacteria, Pasteurellales,
Pasteurellaceae, Pasteurella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.8%; Score 51; DB 16; Length 369;
larity 37.5%; Pred. No. 25;
Conservative 5; Mismatches 8; Indels
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II SELE-Neuroblatoma;

II W.B., Gruber C., Jessee J., Polayes D.;

I'M.B., Gruber C., Jessee J., Polayes D.;

I'M.B., Gruber C., Jessee J., Polayes D.;

Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; BX161420; CAD61894.1;

GO, GO.0046821; Cestrachromosomal DNA; IEA.

InterPro; IPR00310; Ig-1ike.

InterPro; IPR003597; Ig_c1.

InterPro; IPR003697; Ig_MHC.

PEam; PR00407; Ig; 3.

PROSITE; PS50835; IG_LIKE; 3.

PROSITE; PS50290; IG_MHC; 3.
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Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
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Q9CM48 PRELIMINARY; PRT; 369 AA.
Q9CM48;
01-UUN-2001 (TrEMBLrel. 17, Created)
01-UUN-2001 (TrEMBLrel. 17, Last sequence update)
01-UN-2003 (TrEMBLrel. 24, Last annotation update)
MetB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP, P00935; 1CS1.
GO; GO: 0006520; P:amino acid metabolism; IEA.
GO; GO: 0006520; P:amino acid metabolism; IEA.
InterPro; IPR00277; Cyg.Met.Meta_PP.
InterPro; IPR00153; Cyg.Met.Meta_PP.
PROSITE; PS00868; CYS.MET.METAB_PP; 1.
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                                                                                                                                                                                                                                                                                                               STRAIN=Pm70;
MEDLINE=21145866; PubMed=11248100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Neuroblastoma;
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome. SEQUENCE 369 AA;
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                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                           NCBI_TaxID=747;
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                                                                                                                                              METB OR PM0995
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DB 4;

37.8%; Score 51;

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Lehrach H., Poustka A., Lundeberg J.;
"The European IMAGE consortium for integrated Molecular analysis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Human rectum tumor;
Bloecker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
Bloecker H., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX538066; CAD97996.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.8%; Score 51; DB 4; Length 416; 39.1%; Pred. No. 28; cive 5; Mismatches 9; Indels
                Indels
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Planting M., Sumoy L.; Pluvinet R., Estivill X., Escarceller M., Sumoy L.; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                          O9NPP6;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Immunoglobulin heavy chain variant (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DKFZp686K04218 (Fragment)
DKFZP686K04218.
                7:
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                                                                                                                                                                           416 AA
39.1%; Pred. No. 25; tive 7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262 GETFICTAAHPELKTPLIANITK 284
                                                                         220 GERFICTVIHTDLPSPLKQTISR 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 GETYKSTVSHPDLPREVVRSIAK 24
                                                  2 GETYKSTVSHPDLPREVVRSIAK 24
                                                                                                                                                                       PRT;
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Best Local Similarity 39...
Best Word 9, Conservative
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Gaps

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"Isolation of a rat immune response gene identical to an alleged mouse a class II beta-chain pseudogene.";
Immunogenetics 22:601-608(1985).
ENBL; MISSG1, AAA68203.1;
ENBL; MISSG1, AAA68203.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR0078597; Ig-di.
InterPro; IPR00780597; Ig-di.
InterPro; IPR007806; Ig-MHC.
InterPro; IPR00780597; IG-di.
InterPro; IPR00780597; IG-di.
InterPro; IPR00780597; IG-di.
InterPro; IPR00780597; IG-di.
INTERPRO; IRR00780597; IRR00780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37.8%; Score 51; DB 11; Length 341; 45.5%; Pred. No. 23; tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37.8%; Score 51; DB 7; Length 93; 52.9%; Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Indels
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Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       341 341
341 AA; 36450 MW; 7C3D17465CA608CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 AA
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Thromb. Haemost. 69:351-360(1993)
EMBL; D43759; BAA07816.1; -.
HSSP; P02671; 1FZA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Balb/c;
MEDLINE=93269219; PubMed=8497848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 GETYKSTVSHPDLPREV 18
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Matches 10; Conservative
Lernmark A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 52.9
Matches 9, Conservative
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NON TER
SEQUENCE
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Q08284;
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Q08284
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Q9CM48
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01-NOV1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Rat MHC class II RTI.B-beta2 (Fragment).
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chodata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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SEQUENCE FROM N.A.
Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
Mesyanzhinov V.V., Sykilinda N.N., Krylov V.V., Volckaert G.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AF399011, AAL83047.1; -.
InterPro; IPR008160; Collagen.
Pfam, PP01391; Collagen; 2.
SEQUENCE 1093 AA; 115835 MM; D755B6C65D910DF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21914557; PubMed=11916376;
Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
Bourkaltseva M.V., Sykilinda N.N., Krylov V.N., Volckaert G.;
"The genome of bacteriophage phikZ of Pseudomonas aeruginosa.";
J. Mol. Biol. 317:1-19(2002).
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Pseudomonas phage phiKZ.
Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
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38.5%; Score 52; DB 9; Length 1093;
Best Local Similarity 39.1%; Pred. No. 55;
Matches 9; Conservative 8; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 52.9%; Pred. No. 19;
Matches 9; Conservative 3; Mismatches 5; Indels
   sequence of the nematode C.elegans: A platform for
                            investigating biology.";
Science 282:2012-2018 (1998).
BMBL; 292827; CAB07326.1; -.
PIX, T19571. T19571.
WormPep; C29F7.1; CE08442.
InterPro; IPR004112; DUF227.
Pfam; PP02958; DUF227; 1.
SMART; SM00887; CHK; 1.
SMART; SM00887; CHK; 1.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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STRAIN=Wistar, TISSUE=Kidney;
MEDLINE=86084127; PubMed=3865893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                9 VSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 LKHPNLPKNVVIKIASC 76
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Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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STRAIN-ATCC 51449 / 381;
STRAIN-ATCC 51449 / 381;
SUBJINE-22709201; PubMed=12810954;
Suerbaum S., Josenhans C., Sterzenbach T., Drescher B., Brandt P.,
Bell M., Droege M., Fartmann B., Fischer H.-P., Ge Z., Hoerster A.,
Holland R., Klein K., Kenig J., Macko L., Mendz G.L., Nyakatura G.,
Schauer D.B., Shen Z., Weber J., Frosch M., Fox J.G.;
"The complete genome sequence of the carcinogenic bacterium
Helicobacter hepaticus.",
Proc. Natl. Acad. Sci. U.S.A. 100:7901-7906(2003).
EMBL. AEOIT46; AAPT7526.1;
EMBL. AEOIT46; AAPT7526.1;
EMBL. AEOIT46; AAPT7526.1;
EMBL. AEOITAGE.
SEQUENCE 209 AA; 23936 MM; EDOBS0093E84F6FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
Helicobacteraceae; Helicobacter.
NCBI_TaxID=32025;
                                                                                                                                                                                   39.3%; Score 53; DB 13; Length 684; 47.6%; Pred. No. 24; tive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  / Match
Local Similarity 27.3%; Pred. No. 9.4;
lo 5; Conservative 7; Mismatches 9; Indels
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Submitted (MRR-1997) to the EMBL/GenBank/DDBJ databases
                                                         POTENTIAL.
NOVEL ANTIGEN RECEPTOR.
2FF9D2071CDA6DFD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 CGEQYTNTFHHPSQPQAALENNLESIKNCSLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CGETYKSTVSHPDLPR-----EVVRSIAKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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                                                                                                                                                                                                                                                                                                                                                         642 TYSCLVGHPSLNRDLIRSTNK 662
                                                                                                                                                                                                                                                                                                                    4 TYKSTVSHPDLPREVVRSIAK 24
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                                75224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25, 01-OCT-2003 (TrEMBLrel. 25,
PROSITE; PS00290; IG_MHC; 3.
                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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                                                                18
684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter hepaticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein.
                                                                                                                                684 AA;
                                                                                                                                                                                                                     Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                 Receptor, Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C29F7.1 protein.
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                                                                                                                             SEQUENCE
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Matches
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      RA Y E E S
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Nature 374:168-173(1995).
Nature 374:168-173(1995).
BNBL: 018701; AAB48195.1; -.
PIR; S60266; S60266.
HSSP: p01842; Preceptor activity; IEA.
Interpro; IPR0031010; Ig-11ke.
Interpro; IPR003597; Ig-c1.
Interpro; IPR003006; Ig-MHC.
Pfam; PF00047; ig: 6.
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
dinglymostoma cirratum (Nurse shark).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Orectolobiformes;
NCBI_TAXID=7801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,
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TISSUE=Spleen;
MEDLINE=95183140; PubMed=7877689;
Greenberg A.S., Avila D., Hughes M., Hughes A., McKinney E.C.,
Flajnik M.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Haemophilus ducreyi.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=730;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 54; DB 16; Length 599; llarity 46.4%; Pred. No. 14; Conservative 2; Mismatches 9; Indels
                                        9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PARAIN=35000M N.T. Ray W.C., Mahairas G., Sabo P., Mungur Johnson R.S. Jr., Ray W.C., Manairas G., Sabo P., Mungur Johnson L., Nguyen D., Wang J., Forst C., Hood L.; Submitted G.UN-2003) to the EMBL/GenBank/DDBJ databases. EMBL, ARD11155; AAP96386.1; -. Complete preference of Hongur Submitted G.UN-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AE011155; AAP96386.1; -. Submitted Complete Sequence Sequence
                                                                                                                                                                                                                                                                                                                                                  01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
GTP-binding protein LepA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   684 AA
                                                                                                                                                                                                                                                                                                                           599 AA
      Best Local Similarity 46.4%; Pred. No. 3; Matches 13; Conservative 2; Mismatches
                                                                                                  2 GETYK----STVSHPDLPREVVRSIAKC 25
                                                                                                                                       68 GETYQLNFIDTPGHVDFSYEVSRSLAAC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GETYK----STVSHPDLPREVVRSIAKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70 GETYQLNFIDTPGHVDFSYEVSRSLAAC 97
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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SMART; SM00407; IGc1; 4.
PROSITE; PS50835; IG LIKE; 6.
                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
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1090544
100060
AC 009054
DT 001-NN 001-NN
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g

8

ij

Gaps

.. 8

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Database :

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Q91205 mus musculu 08136 mus musculu 08136 mus musculu 04878 arabidopsis Q9602 drosophila Q86nq0 drosophila Q8bwt3 mus musculu Q8bwt3 mus musculu Q8457 proteus vul Q88x57 proteus vul Q88x57 proteus vul Q88x99 bradythizob Q9410 drosophila Q0910 drosophila Q95110 mus musculu Q8510 mus musculu Q8509 mus musculu Q86x57 mus musculu Q9410 musculu Q95100 musculu Q85100 musculu Q95100 musculu Q85100 musculu Q85100 musculu
                             996eyo homo sapien
08wki homo sapien
08wki homo sapien
096ga6 homo sapien
09667 leishmania
00209 caenorhabdi
09ev20 listeria mo
08dffo vherio vuln
08dji 6 streptococc
08dii heliobacill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 520 N. A. S. SEQUENCE FROM N. A. S. STRAIN-SS9;
A. Chi E., Barlett D. H.;
A. Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
R. WEBL; 141669; AAA56230.1; -.
R. PRIS, 170214; A70214; A70214; A70214; A70214; B. RSP, PRIS51; IDAR.
R. GO; GO:0005525; F:GTP binding; IEA.
R. GO; GO:000576; F:translation elongation factor activity; IEA.
R. GO; GO:0006414; P:translational elongation; IEA.
R. InterPro; IPR000795; EF GTPbind.
R. PÉBM; PF00009; GTP_EFTU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Photobacterium profundum (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium.
Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chi E., Bartlett D.H.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15016 MW; 7FCSE05FD6AF1F3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
UNOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
RPOB, LEPA and ORF 2, 3, 4 genes (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         137 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40.0%; Score 54;
                                                                                                                                                                                                                                                                                                                         Q8BWT7
Q8BUF3
Q8BXL3
Q9D9F8
Q8KK57
Q89W99
                                096EY0
096AA6
096AA6
090BA6
002099
09EV2
002099
09EVZ
008DSF
09BSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9DBZ2
Q8JNC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERMY: PRO0009; GTP EFTU; 1.
PRINTS; PRO0315; ELONGAURECT.
GTP-binding; Protein biosynthesis.
NON TER
                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
STRAIN=SS9;
2.84.4
7.89.5
7.00.0
7.00.0
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         057464
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Q57464
 SAN DE LA SERVICIO DEL SERVICIO DE LA SERVICIO DEL SERVICIO DE LA SERVICIO DE LA SERVICIO DE LA SERVICIO DEL SERVICIO
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Q7v173 haemophilus
Q90544 ginglymosto
Q7vhn6 helicobacte
017620 caenorhabdi
Q88d16 pseudomonas
Q31260 rattus norv
Q08284 mus musculu
Q9cm48 pasteurella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q@6ttl homo sapien
Q9npp6 homo sapien
Q72379 homo sapien
Q72374 homo sapien
Q98474 mus musculu
Q8wux4 homo sapien
Q9bul0 homo sapien
                                                                                                                            February 26, 2004, 08:18:11; Search time 31.4 Seconds (without alignments) 251.209 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                                                                                                                                                                  1017041
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                               1017041 seqs, 315518202 residues
                                                                                                                                                                                                 US-09-701-623C-84
135
1 CGETYKSTVSHPDLPREVVRSIAKC 25
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Maximum Match 100%
Listing first 45 summaries
                                                                                           protein search, using sw model
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Q7VL/13
Q7VEN6
Q90544
Q7VEN6
Q082D16
Q082B16
Q082B16
Q082B1
Q907711
Q9077379
Q72374
Q93744
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
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sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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spphage:*
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Maximum DB seq length: 200000000
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sp_bacteria:*
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sp rodent: *
sp_virus: *
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Query
Match Length D
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Result 80.

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMED dustration the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this etatement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE.
INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE).
INTERCHAIN (WITH HEAVY CHAIN IN ANOTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.

NON TER 1 1 1 1 1 1 DOMĀIN 6 98 IG-LIKE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (WITH LIGHT CHAIN) (PROBABLE)
INTERCHAIN (WITH HEAVY CHAIN) (PROBABLE)
Kerr M.A.;
"The structure and function of human IgA.";
Biochem. J. 271:285-296(1990).
-i- FUNCTION: Ig alpha is the major immunoglobulin class in body secretions. It may serve both to defend against local infection and to prevent access of foreign antigens to the general
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH J CHAIN) (PROBABLE)
                                                                                                                             N-LINKED (GLCNAC. ..).
P -> S (IN A2M(2) ALLOTYPE).
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(IN A2M(2) ALLOTYPE).
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/FTId=VAR_003883.
V -> A (IN A2M(2) ALLOTYPE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR 003884.
98922700756F3276 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE 1.
IG-LIKE 2.
IG-LIKE 3.
PROBABLE.
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BER; B223-660; B223-60.
HSP; P01810; 2FBJ.
Genew; HGNC:5479; IGHA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 AA; 36508 MW;
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317
317
101
101
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167
179
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CARBOHYD
CARBOHYD
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CARBOHYD
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Search completed: February 26, 2004, 08:24:23 Job time : 6.4 secs

Query Match
37.8%; Score 51; DB 1; Length 340;
Best Local Similarity 39.1%; Pred. No. 3.6;
Matches 9; Conservative 5; Mismatches 9; Indels

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Gaps

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                         EMBL; AE016748; AA004870.1; -.
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P01877;
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SEQUENCE
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            SPETE WAR BERRARE BERRARE SOLL COCCOCC
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                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is no removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=ATCC 12228;

Dubmdc=12950922;

Diang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,

Qin Z.-Q., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,

Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.,

"Genome-based analysis of virulence genes in a non-biofilm-forming Staphylococcus epidermidis strain (ATCC 12228).",

Mol. Microbiol. 49:1577-1593 (2003).

-i- SIMILARITY: Belongs to the GTP-binding elongation factor family.

LepA subfamily.
  Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
LepA subfamily.
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38.5%; Score 52; DB 1; Length 606;
Best Local Similarity 46.4%; Pred. No. 4.7;
Matches 13; Conservative 1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 27 GTP (BY SIMILARITY).
86 90 GTP (BY SIMILARITY).
140 143 GTP (BY SIMILARITY).
606 AA, 66856 MW, 94FE045B04EEF615 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria, Firmicutes, Bacillales, Staphylococcus, NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-0cT-2003 (Rel. 42, Created)
10-0cT-2003 (Rel. 42, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
LEPA OR SE1271.
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InterPro, IPR000795, EF GTPbind.
InterPro, IPR000640; EFG_C.
InterPro, IPR000629; EFG III V.
InterPro, IPR004161; EFTU D2.
InterPro, IPR004161; EFTU D2.
InterPro, IPR006297; LepA.
InterPro, IPR006297; LepA.
InterPro, IPR006297; EFG_C.
InterPro, IPR00600, Translat_factor.
Pfam; PF00679; BFG_C.1.
Pfam; PF00679; GTP_EFTU; 1.
Pfam; PF00879; TGR01393; JepA; 1.
TIGRFAM; TIGR01393; JepA; 1.
TIGRFAM; TIGR01393; JepA; 1.
TIGRFAM; TIGR01393; JepA; 1.
TIGRFAM; Complete Profeome.
MP_EIND
                                                                                                                                                                                                                                                                                       EMBL; AE005781; AAK23018.1; ALT_INIT.
HSSP; P13551; 1ELO.
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OBCP13;
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NP_BIND
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LEPA_STAEP
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MEDLINE=84130179; PubMed=6421489;
Flanagan J.G., Lefranc M.-P., Rabbitts T.H.;
"Mechanisms of divergence and convergence of the human immunoglobulin alpha 1 and alpha 2 constant region gene sequences.";
cell 36:681-688(1984).
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MEDLINE=78137069; PubMed=416441;
Torano A., Putnam F.W.,
Toranolete amino acid sequence of the alpha 2 heavy chain of a human 19A2 immunoglobulin of the A2m (2) allotype.",
Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE (MYSLOMA PROTEIN LAN).
MEDIJINE=79180146), PUDMed=2862957.
TSUZUKİĞA X., WANG C.-C., PUTLAM. F.W.;
"Structure of the A2m(1) allotype of human IgA -- a recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38.5%; Score 52; DB 1; Length 607; 46.4%; Pred. No. 4.7; Live 1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 27 GTP (BY SIMILARITY).
86 90 GTP (BY SIMILARITY).
140 143 GTP (BY SIMILARITY).
607 AA, 68275 MW, DA714C86IEBCS89F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-JUL-1986 (Rel. 01, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   340 AA
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HAMAD: ME 00011; -1.

ILLERPEO: IRRO00755; EPE GTPbind.

ILLERPEO: IRRO00755; EPE GTPbind.

ILLERPEO: IRRO00640; EFE GTIL V.

ILLERPEO: IRRO00622; EPE TIL V.

ILLERPEO: IRRO0629; EPT D2.

ILLERPEO: IRRO0629; EPT D2.

ILLERPEO: IRRO0629; EPT D2.

PEAM; PPO0009; GTP EFT 1.

PEAM; PPO0149; GTP EFT 1.

PRAYE; PRO0145; ELONGATNECT.

TIGREAMS; TIGRO133; IEPA; 1.

PROSITE; PRO0315; ELONGATNECT.

TIGREAMS; TIGRO0331; EPACTOR GTP; 1.

PROSITE; PRO0315; EFACTOR GTP; 1.

PROSITE; PRO0316; EFACTOR GTP; 1.
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STANDARD;
                                                                                                                                                                                                                                                   Ig mu chain C region.
Canis familiaris (Dog)
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LEPA_CAUCR
ID _LEPA_CAUCR
AC Q9A9F4;
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SEQUENCE
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MEDLINE=990000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                     Gaps
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Science 283:754-759(1998).
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
LepA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of an obligate intracellular pathogen of humans:
                                     4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=813;
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46.4%; Pred. No. 2.3;
tive 2; Mismatches 9; Indels
                                  9; Indels
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 98F67C990196EEC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                               30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
38-FEB-2003 (Rel. 41, Last annotation update)
GTP-binding protein lepA.
LEPA OR CT064.
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PIR; B71561; B71561.

HSSP; P13551; JELO.

HAMPP; MC 00071; -; 1.

InterPro; IPR000795; EF GTPbind.

InterPro; IPR000640; EFG II.

InterPro; IPR00461; EFTU D2.

InterPro; IPR00461; EFTU D2.

InterPro; IPR005225; Small GTP.

InterPro; IPR005207; LepA.

InterPro; IPR005000; Translat factor.

Pfam; PP00679; EFG C; 1.

Pfam; PP00099; GTP EFTU; 1.

Pfam; PP01009; GTP EFTU; 1.

Pfam; PR00314; GTP EFTU; 1.

PRINTS; PR00315; ELONGAINFCT.

TIGRERAMS; TIGR0139; BEDTU D2; 1.

PROSITE; PS00301; EFACTOR GTP; PALSE NEG.

GTP-binding; Complete protecme.
   46.4%; Pred. No. 2.3; ive 2; Mismatches
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                                                                                            2 GETYK----STVSHPDLPREVVRSIAKC 25
                                                                                                                                                          72 GETYELNLIDTPGHVDFSYEVSRSLAAC 99
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Best Local Similarity 46.4
Matches 13; Conservative
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X MEDLINE=78180587; PubMed=653360;

A Wasserman R.L., Capra J.D.;

Interspecies homology for the Fc region of a canine immunoglobulin M: interspecies homology for the IgM class.";

Interspecies homology for the IgM class.";

Science 200:1159-1161(1978).

R PIR, A33131; MHDG.

R PIR, A33131; MHDG.

R RILEPRO; IPR003100; Ig-like.

R InterPro; IPR003597; Ig_C1.

R InterPro; IPR003597; Ig_C1.

R PROSITE; SMOA77; IG_116; 4.

SWART; SWOOTO; IG_116; 4.

R PROSITE; PS50835; IG_LIKE; 4.

R PROSITE; PS50835; IG_LIKE; 4.

R PROSITE; PS50835; IG_MHC, 3.

M M MANIAGIObulin domain; Immunoglobulin C region.
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STAALN=ATCC 19089 / CB15;
MEDLINE=2113698; PubMed=11259647;
Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
Bisen J.A., Heidelberg J.F., Alley M.K.K., Ohta N., Maddock J.R.,
Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
DeBOY R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
Kolnay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,
Utcerback T., Tran K., Wolf A., Vamathevan J., Ernser C.M.,
"Complete genome sequence of Caulobacter crescentus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caulobacter crescentus.
Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
Caulobacteraceae; Caulobacter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    McCumber L.J., Capra J.D.;
"The complete amino-acid sequence of a canine mu chain.";
Mol. Immunol, 16:565-570(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             450 AA; 48895 MW; 9D460DA9D1012F5D CRC64;
MUC CANFA STANDARD; PRT; 450 AA. P01874; 21-JUL-1986 (Rel. 01, Created) 15-JUL-1996 (Rel. 01, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update)
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28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
GTP-Binding protein lepA.
LEPA OR CC1034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 AA
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                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-177 (MOO).
MEDLINE=80077682; PubMed=117299;
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Best Local Similarity 50.0%
Matches 12, Conservative
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GTP (BY SIMILARITY). DOBD7FBE947157DA CRC64;

66538 MW;

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NP BIND
SEQUENCE
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                                                                                                                                                                     RESULT 10
LEPA CHLMU
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
SPECIES=S.typhi, STRAIN=TY2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
                                                                                                                                                                                                                        Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davise R.M., Dowd L., White N., Farrar J., Fritwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;

William S., Mannell B.G.;

Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;

Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 185:2330-2337(2003).
-!- SUBCELLIOLAR LOCATION: PRESENT IN THE CYTOPLASMIC MEMBRANE AND IS
-LOCATION PRESENT SENDERS.
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
'Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                 van Dijl J.M., van den Bergh R., Reversma T., Smith H., Bron S
                                                                                                                            "Molecular cloning of the Salmonella typhimurium lep gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Membrane; GTP-binding, Complete proteome.

NP_BIND 11 18 GTP (BY SIMILARITY).

NP_BIND 77 81 GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, X54933; CAA36655.1; F.
EMBL, AEG2275; CAA02785.1; F.
EMBL, AEG1635; AA067399.1; F.
EMBL, AEG1635; AA067399.1; F.
EMBL, AEG1635; AA067399.1; F.
EMBL, AEG1635; AA067399.1; F.
EMBLAMAP, MF_00071; F.
INCEPPO; IPR000049; EFG CL
INCEPPO; IPR000640; EFG CL
INCEPPO; IPR000640; EFG CL
INCEPPO; IPR006297; EFG ZII V.
INCEPPO; IPR006000; Translat_factor.
Ffam; PF00009; EFG Cl
Ffam; PF00009; EFFG ZI
Ffam; PF00144; GTP_EFTU D2; I.
Ffam; PF00144; GTP_EFTU D2; I.
FFANTYER PR001323; INCEPTU D2; I.
                                                      SEQUENCE OF 565-599 FROM N.A.
SPECIES=S.typhimurium, STRAIN=JM83;
MEDLINE=91066835; PubMed=2250650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIGRFAMS; TIGR01393; lepA; 1.
IIGRFAMS; TIGR00231; small GTP; 1.
PROSITE; PS00301; EFACTOR GTP; 1.
                                                                                                                                                                                     SEQUENCE FROM N.A.
SPECIES=S.typhi; STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608;
                                                                                                                                            Escherichia coli.";
Mol. Gen. Genet. 223:233-240(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE008817; AAL21477.1; -.
                           Nature 413:852-856(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LepA subfamily.
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MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
Muclaic Acids Res. 28:1397-1406(2000).
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
LepA subfamily.
                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chlamydia muridarum.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
NCBI_TaxID=83560;
40.0%; Score 54; DB 1; Length 599; 46.4%; Pred. No. 2.3;
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                                                   Indels
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GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; IEEA355FF60EBF3D CRC64;
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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InterPro; IPR0000795; EF GTPbind.
InterPro; IPR000604; EFG C.
InterPro; IPR000604; EFG C.
InterPro; IPR006161; EFTU D2.
InterPro; IPR005225; Small GTP.
InterPro; IPR005225; Small GTP.
InterPro; IPR0092000; Translat_factor.
Pfam; PF00169; EFG C; 1.
Pfam; PF00169; EFG EFTU; 1.
Pfam; PF00144; GTP EFTU; 1.
PROSTE; PR00315; ELONGATNFCT.
TIGRRAMS; TIGR0133; LepA; 1.
TIGRRAMS; TIGR00231; Small GTP; 1.
PROSTE; PS00301; EFACTOR GTP; PALSE NEG.
GTP-binding; Complete proteome.
                                                      2; Mismatches
                                                                                                          2 GETYK----STVSHPDLPREVVRSIAKC 25
                                                                                                                                         68 GETYQLNFIDTPGHVDFSYEVSRSLAAC 95
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                                                      Conservative
                                                                                                                                                                                                                                                                                                  STANDARD;
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602 AA;
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                            Similarity
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                                                                                                                                                                                                                                                                                            LEPA CHLMU
Q9PKX6;
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NP_BIND
  Query Match
                               Local
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or send an email to license@isb-sib.ch).
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MEDLINE=21534948; PubMed=11677609;
McClelland M., Sanderson K.B., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulyaney E., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TDAVRCSAKTGVGVQDVLERLVRDIPPPEG -> HRRG;
SENRRWCAGRSRTSGARHSAAGS (IN REF. 1 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria, Próteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Salmonella.
NCBL_TaxID=602, 601;
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91E3678557A46D49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HAMP: MOSON; DESCRIPTION.

BCGGENE; BG10529; lepA.

HAMAP: MF_00071; i.E. GTPbind.

InterPro; IPR000054; EFG_C.

InterPro; IPR000051; EFG_T.

InterPro; IPR000529; LepA.

InterPro; IPR005297; LepA.

InterPro; IPR005297; LepA.

InterPro; IPR005297; LepA.

InterPro; IPR005297; LepA.

InterPro; IPR005000; Translat_factor.

Pfam; PF00144; EFFU D.;

Pfam; PF00144; GTP_EFFU D.;

Pfam; PF01144; GTP_EFFU D.;

Pfam; PF00145; EFCONGATNFCT.

TIGRPAMS; TIGR01393; lepA; 1.

TIGRPAMS; TIGR01393; lepA; 1.

PROSITE; PS00301; EFACTOR GTP; 1.

PROSITE; PS00301; EFACTOR GTP; 1.

Membrane; GTP-binding; Complete proteome.

NP_BIND 77 81 GTP (BY SIMILARITY).

NP_BIND 77 81 GTP (BY SIMILARITY).
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28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
GTP-binding protein lepA.
Salmonella typhimurium, and
Salmonella typhim
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                                                                                                                                                                             EMBL, AE000343, AAC75622.1) -.
EMBL, AE016764, AAN81542.1; -.
EMBL, AE005462, AAG57685.1, -.
EMBL, AP012562, BAB36858.1, -.
EMBL, AE015278, AAN4128.1, -.
EMBL, AE016987, AAP17952.1, -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66570 MW;
                                                                                                               K00426; AAA24063.1; -. D64044; BAA10916.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         PIR; A85903, A85903.
PIR; C91058; C91058.
PIR; H65034; BVECLA.
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599 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEPA SALTY P23698;
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                                                                                                                  EMBL; EMBL; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Loca
Matches
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              SOLUTION OF THE SELECT OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=E.COLI, STRAIN=C157.H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Chnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=S.flexneri; STRAIN=301 / Serotype 2a; MEDLINE=22272406; PubMed=12384590; Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H., Yang J., Yang J., Yang G., Wu H., Qu D., Dong J., Sun L., Xue Y., Zhao A., Zhang J., Zhu J., Xan B., Ding K., Chen S., Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y., Chen R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of Shigella flexmeri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
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MEDLINE-88081865; PubMed=2826164;
Kushiro A., Shimizu M., Tomita K.;
Kushiro A., Shimizu M., Tomita K.;
Molecular cloning and sequence determination of the tuf gene coding for the elongation factor Tu of Thermus thermophilus HB8.";
Eur. J. Biochem. 170:39-398(1987).
-!- SUBCELLULAR LOCATION: PRESENT IN THE CYTOPLASMIC MEMBRANE AND IS
ALSO FOUND IN THE PERIPLASM.
-!- MISCELLANBOUS: THE OVERPRODUCTION OF THIS PROTEIN IS LETHAL TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E.COLI.
SIMILARITY: Belongs to the GTP-binding elongation factor family.
LepA subfamily.
SEQUENCE FROM N.A.

SPECIES=E.coli, STRAIN=O157:H7 / EDL933 / ATCC 700927;

SPECIES=E.coli, STRAIN=1206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Perna N.T., Plunkett G. III, Burland V., Mau B., Kirkpatrick H.A.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Kilnk S., Boutin A., Shao Y., Miller L.,

Grocheck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Melch R.A., Blattner F.R.;

"Genome sequence of enterchaemorrhagic Escherichia coli O157:H7.";

Nature 409:529-533(2001).
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GTP-binding membrane protein of Escherichia coli with sequence
homology to initiation factor 2 and elongation factors Tu and G.";
Proc. Natl. Acad. Sci. U.S.A. 82:7500-7504(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a, MEDLINE=22590274; PubMed=12704152; Web J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A., Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY TO GTP-BINDING PROTEINS.
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MEDLINE=86067932; PubMed=2999765;
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SEQUENCE
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LEPA ECOLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDIATE-21145866; PubMed=11248100;
MEDIATE-21145866; PubMed=11248100;
MAY B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
"Complete genomic sequence of Pasteurella multocida Pm70.";
Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
LepA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Pasteurella.
NCBL TaxID=747;
          Query Match
40.0%; Score 54; DB 1; Length 598;
Best Local Similarity 46.4%; Pred. No. 2.3;
Matches 13; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
GTP-Binding protein lepA.
LEPA OR PMO63.
Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 GETYK----STVSHPDLPREVVRSIAKC 25
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  HI0016;
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LEPA_PASMU
TIGR;
DOR NEW YEAR OF THE SOLUTION O
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SEQUENCE FROM N.A.

SPECIES=E.coli; STRAIN=06:H1 / CFT073 / ATCC 700928;

MEDIATE=2288224; Pubmed=1247157;

MEDIATE=2288224; Pubmed=1247157;

MEDIA R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Domnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";

of uropathogenic Escherichia coli.";

Esch. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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SPECIES=E.coli, STRAIN=K12 / MG1655;
SPECIES=E.coli, STRAIN=K12 / MG1655;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               March P.E., Inouye M.;
"Characterization of the lep operon of Bscherichia coli.
Identification of the promoter and the gene upstream of the signal pertidase I dene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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LEPA OR B2569 OR C3093 OR Z3851 OR ECS3435 OR SF2631 OR S2804.
Escherichia coli,
Escherichia coli O6,
Escherichia coli O157:H7, and
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                          40.0%; Score 54; DB 1; Length 598; 46.4%; Pred. No. 2.3;
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SPECIES-E. coli; Strain-K12;
Nashimoto H. Saito N.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                        GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
GTP (BY SIMILARITY).
; 4D41723C2AEBFD10 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEPA ECOLI STANDARD; PRT; 599 AA. P07682; P76590; 01-APR-1988 (Rel. 07, Created) 10-NOV-1997 (Rel. 35, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
40.0%; Score 54; DB
Best Local Similarity 46.4%; Pred. No. 2.3;
Matches 13; Conservative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 GETYQLNFIDTPGHVDFSYEVSRSLAAC 95
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF00144; GTP_EFTU D2; 1.
PRINTS; PR00315; ELOMETWIC D2; 1.
TICRFAMS; TIGR001393; lepA; 1.
TICRFAMS; TIGR00131; small_GTP; 1.
PROSITE; PS00301; ETACTOR GTP; 1.
GTP-binding; Complete profeome.
NP_BIND 77 81 GTP; BY NP_BIND 77 81 GTP; BY NP_BIND 73 81 GTP; BY NP_BIND 73 134 GTP; EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae, Escherichia.
NCBI_TaxID=562, 217992, 83334, 623;
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SPECIES=E.coli; STRAIN=K12;
MEDLINE=85207751; PubMed=2987248;
                                                                                                                                                                                                                                                                                                         131 134 G
598 AA; 66211 MW;
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InterPro; IPR000640;
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                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
LepA subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
Lancet 361:743-749(2003).
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
LepA subfamily.
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Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Proteobacteria, Gammaproteobacteria, Vibrionales,
Vibrionaceae, Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 40.0%; Score 54; DB 1; Length 597; 1 Similarity 46.4%; Pred. No. 2.3; 13; Conservative 2; Mismatches 9; Indels
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77 81 GTP (BY SIMILARITY).
131 134 GTP (BY SIMILARITY).
597 AA, 65914 MW, 34E0EDBFIFCE8864 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
10-0CT-Anding protein lepA.
LEPA OR VV11563.
Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 597 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 GETYQLNFIDTPGHVDFAYEVSRSLAAC 95
                                                                                                                                                                                                                                                                                                                                                                   HAMAD, MP 00071, -; 1.

INTERPRO; IPR000795, EEF GTPbind.
INTERPRO; IPR000640; EFG C.

INTERPRO; IPR0004161; EFFT D2.
INTERPRO; IPR009100; TEMBLAL factor.

Pfam; PF00079; EFG C; 1.

Pfam; PF00079; EFG C; 1.

Pfam; PF00109; GTP EFTU; 1.

PRINTS; PR00115; ELONGAINFCT.

PRINTS; PR00115; ELONGAINFCT.

GTP-binding; Complete proteome.

NP_BIND
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HAMAP; MF_00071; -; 1.
InterPro; IPR000795; EF_GTPbind
                                                                                                                                                                                                                                                                                                                                              EMBL; AP005082; BAC60837.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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LEPA VIBNU
AC Q8DC78;
DT 10-0CT-2003
DX NUBLI DAMPION
CO NICHIAN PROPER
RN (1)
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NP_BIND
SEQUENCE
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                       STITE SOLUTION AND DESCRIPTION OF THE SOLUTION                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
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SIRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95550630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

Rerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,

McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,

Scott J.D., Shirley R., Liu L.I., Glodek A., Kelley J.M.,

Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,

Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,

Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,

Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 269:496-512(1995).
-!- SUBCELLULAR LOCATION: PRESENT IN THE CYTOPLASMIC MEMBRANE AND IS
ALSO FOUND IN THE PERIPLASM (BY SIMILARITY).
-!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
LepA subfamily.
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 597;
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77 81 GTP (BY SIMILARITY).
131 134 GTP (BY SIMILARITY).
597 AA, 65961 MW, 5845994FF33CA245 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.0%; Score 54; DB 1
46.4%; Pred. No. 2.3;
ative 2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 GETYQLNFIDTPGHVDFSYEVSRSLAAC 95
                         InterPro; IPR009022; EFG_III_V.
InterPro; IPR0040161; EFTU_D2.
InterPro; IPR0040161; EFTU_D2.
InterPro; IPR006297; Leph.
InterPro; IPR009000, Translat_factor.
Pfam; PF00679; EFG_C; 1.
Pfam; PF00149; GTP_EFTU; 1.
Pfam; PF00149; GTP_EFTU; 1.
PRINTS; PR00315; ELONGATNFCT.
TIGREAMS; TIGR01393; leph; 1.
TIGREAMS; TIGR01393; leph; 1.
TIGREAMS; TIGR01393; leph; 1.
TIGREAMS; TIGR0231; small GTP; 1.
GTP-binding; Complete proteome.
NP_EIND
EFG_C.
EFG_III_V.
EFTU_D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, U32687, AAC21694.1; -. PIR, 164042, 164042.
HSSP; P13551; 1DAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 46.49
Matches 13; Conservative
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LEPA OR HI0016.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEPA HAEIN
P43729;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NP_BIND
NP_BIND
SEQUENCE
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LEPA HAEIN
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SEQUENCE OF 205-306 FROM N.A.

MEDLINE-82174576; PubMed=6803238;

Hellman L., Pettersson U., Bennich H.;

"Characterization and molecular cloning of the mRNA for the heavy
"Characterization and molecular cloning of the perion of rat immunoglobulin E.";

(epsilon) chain of rat immunoglobulin E.";

Proc. Natl. Acad. Sci. U.S. A. 79:1264-1268(1982).

-: SIMILARITY: Contains 4 immunoglobulin-like domains.
           Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio. Vibrio. Vibrio. TaxID=670;
                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP, P01854, LIGE.

InterPro; IPR007110; Ig-like.

InterPro; IPR003106; Ig-like.

InterPro; IPR003306; Ig_c1.

InterPro; IPR003306; Ig_mHc.

Pfam; PF00047; Igg. 4.

SMART; SM00407; IGG. 1.

PROSITE; PS00290; IG_MHc; 3.

Immunoglobulin domain; Immunoglobulin C region; Repeat.

NON TER

DOMAIN 103 201 IG_LIKE 1.

DOMAIN 103 201 IG_LIKE 3.

DOMAIN 314 414 IG_LIKE 3.

DOMAIN 314 414 IG_LIKE 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48.9%; Score 66; DB 1; Length 429; 52.2%; Pred. No. 0.025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IG-LIKE 1.

IG-LIKE 2.

IG-LIKE 3.

IG-LIKE 4.

R -> N (IN REF. 2).

P -> L (IN REF. 2).

W, D2970B34578A72B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
GTP-Binding protein lepA.
LEPA OR VP2574.
Vibrio parahaemolyticus.
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3; Mismatches
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MEDLINE=83182019; PubMed=6820340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48671 MW;
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les 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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205
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429 AA;
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LEPA_VIBPA
ID LEPA_VIBPA
AC Q87LN7;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
IG epsilon chain C region.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MEDLINE=8364637; PubMed=6292865;
MEDLINE=8364637; PubMed=6292865;
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
"Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                CH1.
CH2.
CH3.
CH4.
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                       R EMBL; X01857; CAA25977.1; --
R EMBL; X01857; CAA25977.1; --
R PIR; A02145; EHMS.
R PIR; A02145; EHMS.
R PIR; A02145; EHMS.
R INTERPOOL I PR0007110; Ig-like.
R INTERPOOL I PR0003507; Ig_Cl.
R INTERPOOL I PR0003507; Ig_Cl.
R INTERPOOL I PR0003507; Ig_MHC.
R RAST; SMO0407; Ig_MHC.
R RAST; SMO0407; Ig_MHC.
R PROSITE; PS00290; IG_MHC, 3.
R PROSITE; PS00290; IG_MHC, 3.
R IMMUNOSIODULIN domain; Immunosiobulin C region; Glycoprotein.
T DOMAIN 91 197 CH1.
T DOMAIN 91 197 CH2.
T DOMAIN 198 304 CH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

48.9%; Score 66; DB 1; Length 421;
Best Local Similarity 52.2%; Pred. No. 0.025;
Matches 12; Conservative 3; Mismatches 8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [2] SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
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421 AA;
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RESULT 3 EPC_RAT

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EPC_MOUSE
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                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is along as its content is in no way entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
M-LINKED (GLCNAC. ..).
M-> L (POSSIBLE POLYMORPHISM).
/FIId=VAR_003885.
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3D-STRUCTURE MODELING.
MEDLINE=87089848; PubMed=3796618;
Padlan B.A., Davies D.R.,
"A model of the For immunoglobulin B.";
MA inmulol. 23:1063-1075(1986).
-1- SIMILARITY: Contains 4 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L00022; AAB59424.1; ALT_INIT
PIR; A22771; EHHU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PDB; IIGE; 15-UIL-92.
PDB; 1FP5; 30-JAN-02.
PDB; 1G84; 16-MAY-01.
PDB; 100V; 18-SEP-02.
Genew; HGNC:5522; IGHE.
MIM; 147180; --
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SEQUENCE OF 1-40; 68-114 AND 427-428 FROM N.A.
MEDLINE=83065234; PubMed=6815656;
Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney , Bell L.O., Gould H.J.,
"Cloning and sequence determination of the gene for the human immunoglobulin epsilon chain expressed in a myeloma cell line."; Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig epsilon chain C region.
IGHE.
                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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EPC HUMAN
P01854;
  EPC_HUMAN
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  RETARARARE REPRETARE REPRE
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Q871n7 vibrio para
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staphylococ
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P07682 P
P23698 E
Q99bxx6 Q99bxx6 Q984067 Q9939f4 Q9939f4 P
Q98513 E
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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MUC HUMAN
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Listing first 45 summaries
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Q8dtf3 streptococc
Q02100 saccharomyc
P01863 mus musculu
P01866 mus musculu
Q8z8a4 salmonella
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xanthomonas
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MEDLINE=83001945; PubMed=6288268;
MAX E.E., Battey J., Ney R., Kirsch I.R., Leder P.;
Duplication and deletion in the human immunoglobulin epsilon genes.";
Cell 29:691-699(1982).
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MEDILTE-8316897; PubMed=6300763;
Seno M., Kuroksawa T., Ono Y., Onda H., Sasada R., Igarashi K.,
Kikuchi M., Sugino Y., Nishida Y., Honjo T.;
"Modecular cloning and nucleotide sequencing of human immunoglobulin
epsilon chain cDNA.";
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MEDLINE=84236029; PubMed=6234164;
Flanagan J.G., Rabbitts T.H.;
"The sequence of a human immunoglobulin epsilon heavy chain constant region gene, and evidence for three non-allelic genes.";
EMBO J. 1:655-660(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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P01865
P01867
Q8pmv3:
Q823h7
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
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PRELIMINARY SEQUENCE (MYELOMA PROTEIN ND)
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LEPA_LACPL
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SKO1_YEAST
GCAA_MOUSE
GCB MOUSE
MODG_SALT!
MODG_SALT!
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GCBM_MOUSE
LEPA_XANAC
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68 GETYQLNFIDTPGHVDFSYEVSRSLAAC 95
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C91058
GTP-binding elongation factor [imported] - Escherichia coli (strain O157:H7, substrain R
C;Species: Escherichia coli
C;Species: N:; Yasunaga, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 9, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C91058
A;Accession: C91058
A;Accession: C91058
A;Accession: C91058
A;Cross-references: GB:BA000007; PIDN:BAB36858.1; PID:g13362906; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Genetics:
A;Ge
A; Residues: 1-599 sELAT>
A; Cross-references: GB:AE000343; GB:U00096; NID:g2367139; PIDN:AAC75622.1; PID:g1788922;
A; Cross-references: GB:AE000343; GB:U00096; NID:g2367139; PIDN:AAC75622.1; PID:g1788922;
A; Experimental source: strain K-12, substrain M01655
B; March, P.E.; Inouye, M.
J. Biol. Chem. 260, 7206-7213, 1985
A; Title: Characterization of the lep operon of Escherichia coli. Identification of the p
A; Reference number: A22627; MUID:85207751; PMID:2987248
A; Reference number: A22627
A; Molecule type: DNA
A; Residues: 1-52, N', 54-155, 'HRRGALFSENRRYCAGRSR', 156, 'SGA', 160, 'H', 162-163, 'AGS', 186-26
A; Residues: 1-52, N', 54-155, 'HRRGALFSENRRYCAGRSR', 156, 'SGA', 160, 'H', 162-163, 'AGS', 186-26
A; Residues: 1-52, N', 54-155, 'HRRGALFSENRRYCAGRSR', 156, 'SGA', 160, 'H', 162-163, 'AGS', 186-26
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A; Residues: 1-52, N', 54-155, 'HRRGALFSENRRYCAGRSR', 160, 'H', 162-163, 'AGS', 186-26
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Cyrp-binding membrane protein lepA - Escherichia coli (strain O157:H7, substrain EDL933)

Cypacies: Escherichia coli

Cybate: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001

Cybacesidon: A85903

Cypacesidon: A85903

Cyperna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
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A,Status: preliminary
A,Molecule type: DNA
A,Rolecule type: DNA
A,Residues: 1-599 <STO>
A,Cross-references: GB:AE005174; NID:g12516987; PIDN:AAG57685.1; GSPDB:GN00145; UWGP:Z38
A,Experimental source: strain O157:H7, substrain EDL933
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A,Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A,Reference number: A85480; MUID:21074935; PMID:11206551
A,Accession: A85903
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Search completed: February 26, 2004, 08:28:17 Job time : 11 secs

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C/Species: Bscherichia coli
C/Species: Bscherichia coli
C/Species: Bscherichia coli
C/Species: Brant-1888 #sequence_revision 05-Dec-1997 #text_change 01-Mar-2002
C/ACCession: H65034; A22627
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.U.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Fittle: The complete genome sequence of Escherichia coli K-12.
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C. Superfamily: GTP-binding membrane protein leph; translation elongation factor Tu homo.
C. Superfamily: GTP-binding; membrane protein; nucleotide binding; P-loop
C. Keywords: GTP binding; membrane protein; nucleotide binding; P-loop
F;5-134/Domain: translation elongation factor Tu homology <ETU>
F;11-18/Region: nucleotide-binding motif A (P-loop)
F;11-18/Region: GTP-binding SAK/L motif
F;162-164/Region: GTP-binding SAK/L motif
F;17,18,53,131,132,134,162/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #st;
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C, Species: Haemophilus influenzae
C, Species: Haemophilus influenzae
C, Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 02-Feb-2001
C, Accession: 164042
R, Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A, Authors Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A, Ritcher Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A, Accession: 164042
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46.4%; Pred. No. 5.2;
tive 2; Mismatches 9; Indels
A, Note: the sequence was determined from the germline gene
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Matches 13; Conservative
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Best Local Similarity 47.6
Matches 10, Conservative
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C; Date: 12-Feb-1998 #sequence_revision outs not shown a; Date: Ig Y heavy chain (7.88) - duck

NiAlternate names: Ig gamma chain (7.88)
C;Species: Anas platyrhynchos (domestic duck)
C;Species: Anas platyrhynchos (domestic duck)
C;Date: 18-Jun-1993 #equence_revision 18-Nov-1994 #text_change 21-Jul-2000
C;Accession: B46529; S20759
R;Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
J; Immunol: 149, 2627-2633, 1992
R;Magor, K.E.; Warr, G.W.; Middleton, D.; Wilson, M.R.; Higgins, D.A.
A;Reference number: A46529; MUD:93017865; PMID:1401901
A;Reference number: A46529; MUD:93017865; PMID:1401901
A;Reference number: B46529
A;Reference number: B46529
A;Reference = RMBL:X65219; NID:g62442; PIDN:CAA46322.1; PID:g62443
A;Residues: 1-572 cMAG>
A;Cross-references: EMBL:X65219; NID:g62442; PIDN:CAA46322.1; PID:g62443
A;Resperimental source: spleen
A;Note: sequence extracted from NCBI backbone (NCBIP:116127)
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: immunoglobulin Pinenology <IMM>
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Best Local Similarity
Matches 12; Conserv
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A; Residues: 1-423 <ISH>
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hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 18 C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Reywords: duplication; glycoprotein; heterotetramer; immunoglobulin
P; 19-80/Domain: immunoglobulin homology < IM2>
P; 223-291/Domain: immunoglobulin homology < IM3>
P; 323-291/Domain: immunoglobulin homology < IM3>
P; 327-398/Pomain: immunoglobulin homology < IM3>
P; 46, 99, 170, 240, 265, 369, 419/Binding site: carbohydrate (Asn) (covalent) #status predicte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ig epsilon chain C region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C;Accession: 838864
R;Kipp, B; Becker, W; Schlaak, M.
R;Kipp, B; Becker, W; Schlaak, M.
A;Kipp, B; Backer, Bata Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of an A;Reference number: 838864
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R;Magor, K.B.; Higgins, D.A.; Middleton, D.L.; Warr, G.W.

Spontten to the EMBL Data Library, March 1994

A;Description: Bridence from duck immunoglobulin genes that IgY is the common ancestor A;Reference number: S43145

A;Accession: S43147
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C;Species: Anas platyrhynchos (domestic duck)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 11-Jan-2000
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A,Residues: 1-548 «KIP»
A,Cross-references: BMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology <IMM>
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A,Molecule type: DNA
A,Residues: 1-110 <MAG>
A,Residues: 1-110 <MAG>
A,Cross-references: BNBL:X78355; NID:g468612; PID:g468613
C,Superfamily: immunoglobulin C region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                 DB 1; Length 429;
0.059;
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48.9%; Score 66; DB 2; Length 548;
Best Local Similarity 52.2%; Pred. No. 0.076;
Matches 12; Conservative 3; Mismatches 8; Indels
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48.9%; Score 66; DB
Best Local Similarity 52.2%; Pred. No. 0.05
Matches 12; Conservative 3; Mismatches
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hes 12; Conserv
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A;Status: preliminary
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Best Local S:
Matches 12,
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B46529
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A; Residues: 1-388 «LIU»
A; Residues: 1-388 «LIU»
A; Cross-references: GB: J00476; NID: g194875; PIDN: AAA38085.1; PID: g387220
C; Crosplex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C; Superfamally: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F; 1-44/Domain: immunoglobulin homology (fragment) «IML»
F; 186-254/Domain: immunoglobulin homology «IM2»
F; 290-361/Domain: immunoglobulin homology «IM3»
F; 290-361/Domain: immunoglobulin homology «IM4»
F; 200-361/Domain: immunoglobulin homology «IM4»
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A;Residues: 'N',169-307,'L',309-342 <KIN>
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
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Cippecies: Rattus norvegicus (Norway rat)
Cipace: 17-Dec-1982 #sequence revision 17-Dec-1982 #text_change 16-Jul-1999
Cipace: 17-Dec-1982 #sequence revision 17-Dec-1982 #text_change 16-Jul-1999
Ridelman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A;Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A;Reference number: A93442; MUID:83064537; PMID:6292865
A;Accession: A93442
A;Residues: 1-429 *cHEL>
A;Accession: A92937; MUID:83182019; PMID:6820340
A;Contents: myeloma IR162
A;Accession: A90937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ig epsilon chain C region (version 1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Mus 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C;Accession: A02144
R;Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A;Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.
A;Reference number: A02144; MUID:83117774; PMID:6818553
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       A;Accession: I68726
A;Atatus: prelimitary; translated from GB/EMBL/DDBJ
A;Actus: prelimitary; translated from GB/EMBL/DDBJ
A;Actus: 1-107 <RES>
A;Residues: 1-107 <RES>
A;Cross-references: GB:N22930; NID:g194455; PIDN:AAA37911.1; PID:g194460
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>
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48.9%; Score 66; DB 1; Length 388;
Best Local Similarity 52.2%; Pred. No. 0.053;
Matches 12; Conservative 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                           8; Indels
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48.9%; Score 66; DB 2;
Best Local Similarity 52.2%; Pred. No. 0.014;
Matches 12; Conservative 3; Mismatches
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A,cres. references: GDB:119335; OMIN:147180
A;Nap position: 14q32.33-14q32.33
A;Map position: 14q32.33-14q32.33
A;Map position: 14q32.33-14q32.33
A;Map position: 14q32.33-14q32.33
A;Introns: 1/i, 104/i, 211/i, 319/1
C;Complex: An immunoglobulin neterotetramer subunit consists of two identical light (kaj hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1:
C;Superfamily: immunoglobulin c region; immunoglobulin homology
C;Reywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunogloby
F;22-87/Domain: immunoglobulin homology <IM3>
F;232-301/Domain: immunoglobulin homology <IM3>
F;34-07/Domain: immunoglobulin homology <IM4>
F;14/Disulfide bonds: interchain (to light chain) #status predicted
F;15-105,29-85,135-193,329-299,345-405/Disulfide bonds: #status predicted
F;21,49,99,146,252,275/Binding site: carbobydyacae (dan) (covalent) #status experimental
F;21,209/Disulfide bonds: interchain (to heavy chain) #status predicted
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R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 27, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid A;Reference number: 154443; MUID:88152907; PMID:3346043
A;Accession: 168730
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
C;Accession: 168726
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
Immunogenetics 77, 288-292, 1988
A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid A;Reference number: 154443; MUID:88152907; PMID:3346043
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C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000
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C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;22-90/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                         compared with conceptual translation
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Pred. No. 0.011;
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                                                                                                                                                                                                     A,Molecule type: DNA
A,Residues: 401-428 <HE3>
A,Cross.references: GB:S53497, NID:g263162; PIDN:AAB24855.1;
A,Experimental source: B cell myeloma U-266
C,Genetics:
                            nurce: B cell myeloma U-266 extracted from NCBI backbone (NCBIP:125299)
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A;Molecule type: mRNA
A;Residues: 1-107 <RES>
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Best Local Similarity 56.5%;
Matches 13; Conservative '
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J. Exp. Med. 176, 233-243, 1992

Ayitie: Two univalid forms of human immunoglobulin E encoded by alternative RNA splicing Ayitie: Two univalid forms of human immunoglobulin E encoded by alternative RNA splicing Ayecession: PRIJ21 will be a splicing and Ayecession: PRIJ21 will be a splicing and Ayecession: PRIJ21 will be a splicing and Ayeritie: MODE and a splicing and Ayeritie: MODE and a splicing and Ayeritie: MODE and a splicing of human immunoglobulin epsilon chat a present a splicing and aucleotide sequencing of human immunoglobulin epsilon chat a present a splicing and aucleotide sequencing of human immunoglobulin epsilon chat a present a splicing and aucleotide sequencing of human immunoglobulin epsilon chat a present a splicing and aucleotide sequencing of human immunoglobulin epsilon chat a present a splicing a splicing and aucleotide sequencing of human immunoglobulin epsilon chat a present a splicing and a splicing and a splicing and a splicing a splicing a splicing and a splicing a splicing and a splicing a splicing and a sequence determined a splicing and a splicing and a splicing a splicing and a splicing a splicing and a sequence determined a splicing and a sequence determined a splicing and a sequence determined a splicing and sequence a splicing a splicing and sequence a splicing a splicing and sequence determined a splicing and sequence a splicing a splicing and sequence a splicing a splicing and sequence a splicing a spl
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A,Accession: 802438
A,Accession: 802438
A,Accession: 802438
A,Reference number: 802438
A,Reference number: 802438
A,Reference number: 8152 aIKE
A,Robang, K., Max, B.E., Chap, H.K.; Saxon, A.
J. Biol. Chem. 269, 456-462, 1994
A,Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces A,Accession: A53116; MUID:94103254; PMID:8276835
A,Status: preliminary
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iftle: Characterization of four novel epsilon chain mRNA and a comparative analysis of Reference number: A46536; MUID:93122085; PMID:8419166
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A/Residues: 320-428 < ZH2>
A/Rociscule type: mRNA
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Cispecies: Homo sapiens (man)
Cispecies: J1-Mar-1981
Secrees: J2-Mar-1981
Cibace: J3-Mar-1981
Cibacesion: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C4
Cibacesion: A22771; A23195; PH1214; A93491; A90824; A94418; B93933; S02438; A53116; C4
R;Flanagan, J.G.; Rabbitts, T.H.
EMBO J. 1, 655-660, 1982
A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gen A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gen A;Reference number: A22771; MJID:84236029; PMID:6234164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 103/1; 209/1; 317/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;336-405/Domain: immunoglobulin homology <IMM>
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54.8%; Score 74; DB 2; Length 426;
Best Local Similarity 60.9%; Pred. No. 0.0037;
Matches 14; Conservative 3; Mismatches 6; Indels
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A;Residues: 2-428 «UED>
A;Cross references: GB.J00222; NID:g184755
R;Zhang, K.; Saxon, A.; Max, E.E.
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Ig chain C3 regio
Ig chain C3 regio
Ig epsilon chain C
Ig upsilon chain C
Ig upsilon chain C
Ig upsilon chain C
Ig upsilon chain C
Ig vesilon chain C
Ig vesilon chain C
Ig vesilon chain C
Ig Portein homol
Ig epsilon chain C
Ig Portein chain C
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Ig mu chain C regi
Ig mu chain C regi
Ig mu chain C regi
Ig alpha-2 chain C
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 CGETYKSTVSHPDLPREVVRSIAKC 25
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Maximum Match 100%
Listing first 45 summaries
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EHHU

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168730
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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2: pir2:*
3: pir3:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   \mathsf{GOOOOOOOO} = \mathsf{GWOWWWW}
                                                                                                                                                                                                                                                     Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                     Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Result
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Gaps

Ig mu chain C regiug mu chain C regiug mu chain C regiug mu chain C regiug heavy chain - hugh mu chain C regiug mu chain C regiug mu chain C regiug mu chain Drotei probable (TP-bindia) Ig mu chain precur hypothetical protei Ig gamma 1 chain c gramma 1 chain c a chai	ALIGNMENTS  IS6948  Ig epsilon-chain - chimpanzee (fragment)  Ig epsilon-chain - chimpanzee (fragment)  C. Date: 04-0ct-1996 #sequence_revision 04-0ct-1996 #text_change 21-Jan-2000  C. Accession: 136948  R. Sakoyama, Y.; Hong, K.  A; Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangut.  A; Reference number: 136948; MUID:87147136; PMID:3103123  A; Residues: 136948; MUID:87147136; PMID:3103123  A; Molecule type: DNA  A; Molecule type: DNA  A; Moscass-references: GB:MIS398; NID:g176797; PIDN:AAA35416.1; PID:g176798
	ALIGNMENTS ent) ee) on 04-Oct-1 80-1084, 19 unoglobulin 47196; PMID om GB/EMBL/
\$33768 \$03961 \$03961 \$03961 \$0361 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0301 \$0	ALI ragment panzee) vision , 1080- immunc :871471 d from
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4 4 4 4 4 4 4 4 11 13 13 8 8 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9	mpanzee ytes (c equence K. K. A. U.S.A. U.S.A. Quences 6948; M transl
000000000000400000	chi lodi gi, se se se rry; rry; ci.
$\begin{array}{c} \mathbf{G} \\ $	e e e e e e e e e e e e e e e e e e e
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ALIGNMENTS  IS6948  Ig epsilon-chain - chimpanzee (fragment) C;Species: Pen troglodytes (chimpanzee) C;Species: Pen troglodytes (chimpanzee) C;Species: 136948 C;Accession: 136948 Exc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987 Exc. Natl. Acad. Sci. Natl. Natl. 136948; MUID:87147196; PMID:310 Exc. Natl. Acad. Sci. Natl. Nat
66 66 66 66 66 66 66 66 66 66 66 66 66	REGULT 1 136948 19 epsilon- (Species: (C, Accession R, Sakoyama, Proc. A, Title: Nu, A, Accession A, Reference A, Molecule

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Search completed: February 26, 2004, 08:29:27
Job time : 13.6 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.08
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: peptide US-09-303-323-101
                COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                      Length 42
                                                                          10; Indels
                                  Query Match
45.7%; Score 64; DB 4;
Best Local Similarity 48.0%; Pred. No. 0.0064;
Matches 12; Conservative 3; Mismatches 1
                                                                                                                                                                                                                                     Sequence 101, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOGENS
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
COTTY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 101, Application US/09303323

Patent No. 6228987

GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: IMMUNOGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan, & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
SOFTWARE:
SOFTWARE:
RPILICATION NUMBER:
FILING DATE:
FILING DATE:
ATTORNEY/AGENT INPORMATION:
NAME:
MATIA H. LIN
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECHONE:
TELECHONE:
212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Morgan & Finnegan, L.L.P.
345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 CGETYQSRVTHPHLPRALMRSTTKC 45
                                                                                                             1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                   18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-4148-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 32.
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US-09-100-414B-101
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US-09-303-323-101
US-09-770-014-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
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COMPUTER READABLE FURM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIPICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/COCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SIZ-758-6490
INFORMATION FOR SEQ ID NO: 101:
CONTENDE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGYGYQSIVDRPDFPKPIVRSITLC 25
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48.0%; Pred. No. 0.0064;
Live 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-09-770-014-100
Sequence 100, Application US/09770014
FALENCE NO. 6559282
GENERAL INFORMATION:
APPLICATING WAND Chang Yi
TITLE OF INVENTION: INMUNOSENS
TITLE OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: MOTGAN E.L.P.
                                        PFLICALLON
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: 212-758-4800
TELEFRAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CGYGYOSIVDRPDFPKPIVRSITLC 25
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TOWNTH: 42 amino acids
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SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: INWINGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSES: MORGAN E.I.P.
STREET: 345 Park Avenue
CONTY: New York
                                                     Sequence 98, Application US/09770014

Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: INMUNOGENS
TITLE OF INVENTION: INMUNOGENS
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STRRET: 345 Park Avenue
CITY: New York
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGYGYQSIVDRPDFPKPIVRSITLC 25
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                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC.Windows OPERATING SYSTEM: Word 97 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/770,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGRNT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REPERRORE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
COMPUTER: IBM PC competible
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible SYSTEM: PC.Windows
                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 42 amino acids
amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                         RESULT 11
US-09-770-014-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-770-014-99
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                                                                                                                                                                                                                                                                                             Query Match 45.7%; Score 64; DB 3; Length 42; Best Local Similarity 48.0%; Pred. No. 0.0064; Matches 12; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 35 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFFCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-UNNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAITH H. LIN
RESISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-756-4800
TELEPHONE: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                        1 CGYGYOSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                  18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JS-09-303-323-100
; Sequence 100, Application US/09303323
; Patent No. 6228997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 10154-0054
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
SOFTWARE: Word 97
                            REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-480
TELEFAX: 212-758-6849
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
         REGISTRATION NUMBER: 29,323
                                                                                                                                                          TYPE: amino acid, TOPOLOGY: linear, MOLECTLE TYPE: peptide US-09-303-323-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
GY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-303-323-100
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48.0%; Pred. No. 0.0064;
tive 3; Mismatches 10; Indels
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
COUNTY: USA
ZIP: 10154-0054
ZIP: 10154-0054
ZIP: 10154-0054
ZOWPUTER READABLE FORM:
MODIUM TYPE: FLOPPY disk
COMPUTER: DAN PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFFWARE: WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FLING DATE: 20-JUNE-1999
CLASSIFICATION UNMBER: 29/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
WYNE: WIND ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: INMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSES: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION UNHER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIPICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CGYGYQSIVDRPDFPKPIVRSITLC 25
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APPLICATION NUMBER: 09/100,414
PILING DATE: 20-UUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 99, Application US/09303323
Patent No. 6228987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 48.0°
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide US-09-303-323-98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
GY: linear
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                                                                                                                                                Score 64; DB 3; Length 42;
Pred. No. 0.0064;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 100, Application US/09100414B
; GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS: 106
COUNTRY: Naw York
STATE: NY
COUNTRY: USA
ZIP: 10144-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM FC Compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CUMPUTER NAPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPROME: 212-28-4800
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Patent No. 6228987
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TILLE OF INVENTION: NOVEL LHRH PEPTIDE
TILLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGYGYQSIVDRPDFPKPIVRSITLC 25
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                                                                                                                                                                                                                                                      1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                   18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                   Query Match
Best Local Similarity 48.0%;
Matches 12; Conservative
: LENGTH: 42 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: peptide

US-09-100-4148-99
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-100
                                                                                                                                                                                                                                                                                                                                                                                                       US-09-100-414B-100
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US-09-303-323-98
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Best Local Similarity 48.0%; Pred. No. 0.0064;
Matches 12; Conservative 3; Mismatches 10; Indels
                                                                                           COUNTRY: USA

ZIP: 10154-054
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-UNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEFONNINICATION INFORMATION:
TELEFONNINICATION INFORMATION:
TELEFONNINICATION OF SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
LINFORMATION FOR SEQ ID NO: 98:
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: APPL: POPOLLOGY: linear
INS-09-100-414B-98
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US-09-100-414B-99

Sequence 99, Application US/09100414B

PERTENT NO. 6025468

GENERAL INFORMATION:
APPLICANT: WAIG, Chang Yi
TITLE OF INVENTION: IMMUNOGENS

NUMBER OF SEQUENCES: 106

CORRESONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STATE: New York
STATE: New York
COUNTRY: New York
COUNTRY: USA
ZIP: 10154-0054

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC compatible
OPERATING SYSTEM: PC compatible
OPERATION SYSTEM: PC COUNE-1998

CLASSIFICATION NUMBER: US/09/100,414B
FILING DATE: ACA
ATTORNEY AGENT INFORMATION:
NAME: MAAIA H. LIN
REGISTRATION NUMBER: 29,323
REFERRNCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION NUMBER: 1151-4157
  ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 CGETYÓSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGYGYQSIVDRPDFPKPIVRSITLC 25
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Gaps

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Query Match 45.7%; Score 64; DB 3; Length 25; Best Local Similarity 48.0%; Pred. No. 0.0036; Matches 12; Conservative 3; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-09-100-414B-98
US-09-100-414B-98
Sequence 98, Application US/09100414B
Patent No. 6025468
CENERAL INFORMATION
APPLICANT: Wang, Chang Yi
ITILE OF INVENTION: NOVEL LHRH PEPTIDE
ITILE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICAMT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
STREET: NY
                                                                                                                                              1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                          1 cderýcskýthPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGBNT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-41:
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-756-4800
                                                                                                                                                                                                                                                                                   US-09-770-014-95; Sequence 95, Application US/09770014; Patent No. 6559282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: peptide US-09-770-014-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
GY: linear
         US-09-303-323-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 45.7%; Score 64; DB 3; Length 25; Best Local Similarity 48.0%; Pred. No. 0.0036; Matches 12; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 95, Application US/09303323
Sequence 95, Application US/09303323
Sequence 95, Application US/09303323
Taten No. 6228987
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF SEQUENCES: 106
CORRESPONDENCE ADDRESS: 106
STREET: 345 Park Avenue
CITY: New York
STREET: 345 Park Avenue
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: NOCH 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATION SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILLING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTONNEY, AGBNT INFORMATION:
NAME: MARIA H. Lin
REGISTRATION NUMBER: 29,323
REPRERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTER STICS:
LINGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGYGYQSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGETYOSRVTHPHLPRALMRSTTKC 25
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PRIOR APPLICATION DATA
PRIOR APPLICATION DATE:
FILING DATE: 20-UNE-1998
ATTORNAY/ASENT IRFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/OCCET NUMBER: 1151
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 99
SEQUENCE CHRACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear;
MOLECULE TYPE: peptide
US-09-100-414B-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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GY: linear
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JS-09-192-545-2
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TYPE: PRT
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000000000000000444444
00010000000000444444
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                                                         .; Search time 12.6 Seconds (without alignments)
102.432 Million cell updates/sec
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Sequence
Sequence
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Sequence
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Sequence
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        GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                           US-09-100-414B-95
US-09-303-323-95
US-09-100-414B-99
US-09-100-414B-99
US-09-303-323-99
US-09-303-323-99
US-09-303-323-99
US-09-303-323-99
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US-09-700-414B-97
US-09-700-414B-97
US-09-700-414B-97
US-09-700-414B-97
US-09-700-414B-97
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US-09-770-014-102
US-09-479-614-14
US-09-479-614-2
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140
1 CGYGYQSIVDRPDFPRPIVRSITLC 25
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                                                          February 26, 2004, 08:19:31
                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        - protein search, using sw model
                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                   Length
              Copyright
                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                          Query
                                                                                                   Perfect score:
                                                                                                                             Scoring table:
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                                        OM protein
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                                                                                                              Seguence:
                                                                                                                                                      Searched:
                                                          Run on:
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9, Appli
13, Appl
17334, A
20542, A
210942, A
4258, Ap
2, Appli
2, Appli
                                                                                                            7663, Ap
39, Appl
12582, A
2, Appli
2, Appli
2376, Ap
131, App
                        Sequence
Sequence
Sequence
Sequence
Sequence
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Sequence
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Sequence
Sequence
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Sequence
Sequence
  Seguence
              Sequence
                      US-09-187-049-13
US-09-252-991A-17334
US-09-252-991A-200542
US-09-252-991A-200542
US-09-543-681A-4258
US-08-336-581-2
PCT-US95-13795-2
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US-09-489-039A-12582
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US-09-489-039A-12582
US-09-489-039A-12582
US-09-417-197-133
.09-252-991A-25458
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## ALIGNMENTS

```
APPLICANT: Karasuyama, Hajime
APPLICANT: Karasuyama, Hajime
APPLICANT: Yonekawa, Hiromichi
APPLICANT: Taya, Choji
APPLICANT: Taya, Choji
APPLICANT: Matsucka, Kunie
TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
FILE REPERENCE: 199979270
CURRENT APPLICATION NUMBER: US/09/192,545
CURRENT FILING DATE: 1998-11-13
EARLIER FILING DATE: 1997-11-14
NUMBER OF SEQ ID NOS: 12
SCOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE: Description of Artificial Sequence: Designed heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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82.9%; Score 116; DB 3; L
Best Local Similarity 91.3%; Pred. No. 1.3e-09;
Matches 21; Conservative 1; Mismatches 1;
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Sequence 95, Application US/09100414B
Seneral INFORMATION:
TITLE OF INVENTION: IMMUNOGENS
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STATE: NY
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
CONPUTER READABLE FORM:
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Sequence 2, Application US/09192545
Patent No. 6118044
GENERAL INFORMATION:
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Gaps

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Indels

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APPLICANT: Moresy, Mohamad A.
TITLE OF INVENTION: NO. US20030096369Al-anaphylactogenic IgE vaccines
FILE REPERENCE: PCIIOLA.
CURRENT APPLICATION NUMBER: US/10/152,190
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 28
SOFWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.7%; Score 85; DB 14; Length 114;
llarity 77.3%; Pred. No. 2.9e-05;
Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE: SYNTHETICALLY GENERATED PROTEINS (COLOR OF 401-636-2)
     Best Local Similarity 90.9%; Fred. No. 6.5e-08; Matches 20; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60.7%; Score 85; DB 9; Le tilarity 77.3%; Pred. No. 9.8e-05; Conservative 0; Mismatches 5;
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US-09-401-636-2
Sequence 2, Application US/09401636
Patent No. US20010038843A1
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE REFREENCE: 10223/006001
CURRENT FILING DATE: 1999-02-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1999-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 GEGYÓCRVDHPHFPKPIVRSIT 105
                                                                                                                                    190 GYGYÇCIVDHPDFPKPIVRSIF 211
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                                                                                   2 GYGYQSIVDRPDFPKPIVRSIT 23
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 17; Conserva
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nes 17; Conserva
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CH3
CRANISM: Rat CH3
US-10-152-190-5
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US-10-152-190-5
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Best Local S
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Sequence 2. Application US/10096840D

Publication No. US20030158390A1

GENERAL INFORMATION:

APPLICANT: YISSUM Research Development Company of the Hebrew University of Jerusalem

TITLE OF INVENTION: PEE-PE CHIMERIC PROTEIN FOR TARGETED TREATMENT OF ALLEROY RESPONS

TITLE OF INVENTION: METHOD FOR ITS PRODUCTION AND PHARMACEUTICAL COMPOSITIONS CONTAINERENT APPLICATION NUMBER: US/10/096,840D

CURRENT APPLICATION NUMBER: US/10/096,840D

CURRENT FILING DATE: 1995-12-18

PRIOR FILING DATE: 1995-12-18

PRIOR FILING DATE: 1996-12-18

PRIOR FILING DATE: 1996-12-18

PRIOR FILING DATE: 1996-12-18

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATCHTION NUMBER: DCT / IL96 / 00181

PRIOR FILING DATE: 1996-12-18

SOFTWARE: PATCHTION NUMBER: DCT / IL96 / 00181

PRIOR FILING DATE: 1996-12-18

SOFTWARE: PATCHTION NUMBER: DCT / IL96 / 00181

PRIOR FILING DATE: 1996-12-18

SOFTWARE: PATCHTION NUMBER: DCT / IL96 / 00181

PRIOR FILING DATE: 1996-12-18

SOFTWARE: PATCHTION NUMBER: DCT / IL96 / 00181
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Sequence 4, Application US/10096840D

Publication No. US20030158390A1

GENERAL INFORMATION:

TITLE OF INVENTION: FCe-PR CHIMERIC PROTEIN FOR TARGETED TREAPMENT OF ALLERGY RESPONS

TITLE OF INVENTION: METHOD FOR ITS PRODUCTION AND PHARMACEUTICAL COMPOSITIONS CONTAINED FILE REFERENCE: 1268-067A

CURRENT APPLICATION NUMBER: US/10/096,840D

CURRENT FILING DATE: 1993-03-03-03

PRIOR PILING DATE: 1995-12-18

PRIOR FILING DATE: 1998-06-18

PRIOR PLING DATE: 1998-06-18

PRIOR PLING DATE: 1998-12-18

PRIOR PLING DATE: 1998-12-18

NUMBER OF SEQ ID NOS: 8

SOFTWARE FOR SEQ ID NOS: 8

SOFTWARE FOR SEQ ID NOS: 8
; OTHER INFORMATION: Murine IgE heavy chain, domains C1, C2, C3, C4, and MIGIS fragmen; OTHER INFORMATION: t
US-09-949-375A-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                          Query Match 77.1%; Score 108; DB 9; Length 432; Best Local Similarity 90.9%; Pred. No. 4e-08; Matches 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                         280 GYGYQCIVDHPDFPKPIVRSIT 301
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; ORGANISM: Pseudomonas aeruginosa
US-10-096-840D-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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; ORGANISM: Mouse
US-10-096-840D-2
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US-10-096-840D-2
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LENGTH: 676
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Length 676;

DB 14;

77.1%; Score 108;

Query Match

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Length 340;

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FEATURE:
; OTHER INFORMATION: Peptide antigen
US-10-144-188-14
                       SOFTWARE: Patentin version 3.1
SEQ ID NO 31
LENGTH: 421
TYPE: PRT
CAGANIEM: Mouse (Mus musculus)
US-10-214-524-31
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ORGANISM: Artificial Sequence
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     NUMBER OF SEQ
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APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: And Stankiewicz, Theresa J.
APPLICANT: Chen, Zhowicz, Theresa J.
CURRENT APPLICATION: INMURER: US/10/214,524
CURRENT APPLICATION NUMBER: US/10/214,524
PRIOR APPLICATION NUMBER: 600/312,120
PRIOR FILING DATE: 2001-09-13
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OTHER INFORMATION: Murine IGE heavy chain domains C1, C2, C3, and C4.
US-09-949-375A-28
                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: 21. US-09-949-375A-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.1%; Score 108; DB 9; Length 343; 90.9%; Pred. No. 3.1e-08; Live 0; Mismatches 2; Indels
               Sequence 22, Application US/09949375A
Patent No. US20020172673A1
GENERAL INFORMATION:
APPLICAMT: KLYSNER, Steen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
FILE REPRENCE: 3631.0111P
CURRENT APPLICATION UNBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2.2
IENGTH: 343
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US-09-949-375A-28
Sequence 28, Application US/09949375A
Sequence 28, Application US/09949375A
PERCENT NO. US20020172673A1
GENERAL INFORMATION:
TITLE OF INVERTION: METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION UNMERF: US/09/949,375A
CURRENT APPLICATION UNMERF: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFUTARE: Patentin version 3.1
SEQ ID NO 28
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; Publication No. US20030073142A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.9
Matches 20; Conservative
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US-09-949-375A-22
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US-10-214-524-31
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Sequence 14, Application US/10144188

Sequence 14, Application US/2030170212A1

GENERAL INFORMATION:

APPLICANT: Cai, Zeling

APPLICANT: Shi, Weixing

CURRENT FOR INVENTION: Ex No. US20030170212A1-Tumor Antigens To Treat Autohmmune And

FILE OF INVENTION: FOR NO. US20030170212A1-Tumor Antigens To Treat Autohmmune And

FILE REFERENCE: PRIO10 OrT-1627

CURRENT APPLICATION NUMBER: 05/10/144,188

CURRENT APPLICATION NUMBER: 60/291,300

PRIOR APPLICATION NUMBER: 60/291,300

PRIOR FILING DATE: 2001-05-15

NUMBER OF SEQ ID NOS: 60

SOFTWARE Patentin version 3.2

SEQ ID NO 14

LENGTH: 421
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77.1%; Score 108; DB 14; Length 421;
Best Local Similarity 90.9%; Pred. No. 3.9e-08;
Matches 20; Conservative 0; Mismatches 2; Indels (
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Sequence 19, Application US/09949375A
Fedent No. US20020172673A1
GENERAL INFORMATION: Seen et al.
APPLICAMY: ATXSNER, Seen et al.
TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PATENTIN VEYBION 3.1
SEQ ID NO 199
LENGTH: 432
                                                                                                                                                                              280 GYGYQCIVDHPDFPKPIVRSIT 301
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206 GYGYQCIVDHPDFPKPIVRSIT 227
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                                                                                             2 GYGYQSIVDRPDFPKPIVRSIT 23
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         Query Match
Best Local Similarity 90.9%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: mus musculus
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Best Local Similarity
Matches 20; Conserv
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                                                                                                                                                                                                                     ; OTHER INFORMATION: Artificial amino acid sequence of SEQ ID NO: US-09-949-375A-25
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US-09-40-375A-27
Sequence 27, Application US/09949375A
Sequence 27, Application US/09949375A
Patent No. US20020172673A1
GENERAL INFORMATION:
APPLICANT: KLYSURR, Steen et al.
TITLE OF INTERNITION: METHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 3631-0111P
CURRENT PILLING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 332
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Output INFORMATION: Synthetically generated proteins US-09-401-636-6
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Patent No. US20010038843A1
GENERAL INFORMATION:
TITLE OF INVENTION: ENHANCED VACCINES
FILE REPERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR PILING DATE: 1999-10-22
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION NUMBER: US/09/949,375A
CURRENT FILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 332
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FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
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US-09-401-636-6
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FEATURE:
NAME/KEY: MISC_FEATURE
OTHER INFORMATION: Murine IgE heavy chain, domains C2, C3, C4, and MIGIS fragment
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Score 108; DB 9; Length 341;
Pred. No. 3.1e-08;
0; Mismatches 2; Indels
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| Sequence 20. Application US/09949375A
| Patent No. US20020172673A1
| GENERAL INFORMATION:
| APPLICANT: KLYSNER, Steen et al. |
| TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE |
| TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE |
| CURRENT APPLICATION NUMBER: US/09/949,375A. |
| CURRENT FILING DATE: 2002-01-18 |
| NUMBER: OF SEQ ID NOS: 38 |
| SOFTWARE: PATENTIN Version 3.1 |
| SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetically generated proteins US-10-176-664-6
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                                                                                                                                                                                                                     US-10-176-664-6
US-10-176-664-6
US-10-176-664-6
Sequence 6, Application US/10176664
Sequence 6, Application US/10176664
PUDLICATION NO. US20030031663A1
GENERAL INFORMATION:
TAPPLICANT: Hellman, Lars T.
TILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,6664
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR APPLICATION NUMBER: US/09/401,636
PRIOR PILING DATE: 1999-01-02
NUMBER OF SEQ ID NOS: 11
SOUTHARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 341
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Sequence 28, Appl
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Sequence 2, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 2, Appli
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Sequence 25, Appl
Sequence 27, Appl
Sequence 6, Appli
Sequence 20, Appl
Sequence 22, Appl
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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9 US-09-949-375A-20

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14 US-10-14-188-14

9 US-09-949-375A-28

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9 US-09-949-375A-28

14 US-10-096-840D-2

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15 US-09-9401-636-2
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                                                                                                                                                                                                   809742 seqs, 211153259 residues
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1 CGYGYQSIVDRPDFPRPIVRSITLC 25
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Maximum Match 100%
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us-09-701-623c-8.rag

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The invention relates to a method of producing cytotoxic T lymphocytes (TILS) specific for one or more non-tumour self antigen T cell epitopes. The method involves loading antigen presenting cells (APCS) having class I major histocompatibility complex molecules with the T cell epitopes, and culturing the CD8+ T cells with the APCS to activate precursor CD8+ T cells specific for the T cell epitopes. The invention is useful for treating autoimmune disease including rheumatoid arthritis, psoriasis, insulin dependent diabetes, Crohn's disease, inclimmune thyroiditis, insulin dependent diabetes, Crohn's disease, inclimmantory bowel disease, graft versus host disease and transplant rejection and/or allergic disease such as food allergy, hay fever, allergic rhinitis, allergic asthma and venom allergy. The invention is also useful in cell therapy. The present sequence is mouse immunoglobulin E (IGE). This protein is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Producing cytotoxic T lymphocytes for treating e.g. autoimmune diseases, comprises culturing CD8+ T cells with antigen presenting cells to activate precursor CD8+ T cells specific for T the cell epitopes.
                                                                                                                                                                          Cytotoxic T lymphocyte; CTL; tumour; antigen presenting cell; allergy; lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis; psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever; inflammatory bowel disease; insulin dependent diabetes; cell therapy; crohn's disease; allergic thinitis; graft versus host disease; asthma; transplant rejection; mouse; immunoglobulin E; IGE.
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                     AAE35016 standard; protein; 421 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-MAY-2001; 2001US-0291300P.
                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAY-2002; 2002WO-US015341
                                                                                                                                        Mouse immunoglobulin E (IgE)
                                                                                                 (first entry)
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2 GYGYQSIVDRPDFPKPIVRSIT 23

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Score 108; DB 5; Length 421;
Pred. No. 3.6e-08;
0; Mismatches 2; Indels
                                                    Mouse IgE heavy chain C1-C2-C3-C4 domains.
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                                                                                                                                                                                                                                                                                                                                                                                                             280 GYGYQCIVDHPDFPKPIVRSIT 301
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            AAU80300 standard; protein; 421 AA
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                                                                                                                                          36-SEP-2001; 2001WO-DK000579.
                                                                                                                                                                                        Klysner S, Von Hoegen P,
                                       (first entry)
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                                                                                                                                                                          (PHAR-) PHARMEXA AS.
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Best Local Similarity
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                                      30-JUL-2002
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ABP96586
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AC ABP96
Matches
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Identifying peptides that induce cytotoxic T-lymphocyte, CTL response against IgE, by identifying peptide eliciting CTL response to IgE peptides naturally presented by major histocompatibility complex class I
                                                                                                 Immunoglobulin E; vaccine; IgE; cytotoxic T lymphocyte response; immune response; major histocompatibility complex; MHC; immunogenic; antiallergic; antiasthmatic; immunosuppressive; vasotropic; cytostatic; dermatological; antiinflammatory; IgE-mediated condition; food allergy; atopic hypersensitivity condition; allergic rhinitis; allergic asthma; atopic dermatitis; non-atopic hypersensitivity condition; anaphylaxis;
                                                             Mouse IgE heavy chain amino acid sequence SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Page 160-162; 187pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang Y, Barankiewicz T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-2001; 2001US-0312120P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IGET-) IGE THERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                      08-AUG-2002; 2002WO-US026986.
                    (first entry)
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                    28-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
  This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic I lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell cpitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic thinitis, asthma and atopic dermatitis. The present sequence represents the mouse IgE heavy chain C1-C2-C3-C4 domains used to create the epitopes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.
                                                                                                                                                                                                                                                                                              IgE; allergy; mouse; antiallergic; immunosuppressive; antianaphylactic; antiasthmatic; dermatological; antiinflammatory; immunoglobulin E; IgE; vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis; heavy chain C domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Voldborg B,
GYGYQCIVDHPDFPKPIVRSIT 268
                    247
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Chen Z;

The present invention describes a method (M1) for identifying peptides that induce cytotoxic T-lymphocyte (CTL) response against immunoglobulin E (IgE), comprising providing a test peptide (T) suspected of being able to bind to major histocompatibility complex (MHC) class I molecule, and evaluating (T) for ability to elicit in a mammal a CTL response to naturally processed and presented IgE peptides, where a peptide that induces such a response is identified. Also described are compositions: (C1) comprising at least one immunogenic peptide (I) identified by (M1); (C2) comprising at least one isolated polynucleotide encoding (I); and (C3) comprising at least one isolated polynucleotide encoding (I); and (C3) comprising antigen-presenting cells that recognise at least one (I) where C1-3 are able to bind to at least one MHC class I molecule and to elicit in a mammal a CTL response to naturally processed and presented IgE peptides. (I-3 have antialleratic, antiasthmatic, immunosuppressive, vasorropic, dermatological, antianifiammatory and cytostatic activities, and can be used as inducers of a CTL response against IgE, and in n vaccines. (I-3 are useful for modulating an IgE-mediated condition in a mammal. C1-3 are useful for modulating an IgE-mediated condition in a mammal. C1-3 are training attopic Mypersensitivity condition, IgE mediated attopic Appersensitivity condition, IgE-mediated non-atopic constitution and presented condition as allergic constitution as allergic condition as allergic condition as allergic. ö rhinitis, allergic asthma, food allergies, or atopic dermatitis), non-atopic hypersensitivity conditions (such as anaphylaxis, and urticaria hives). The present sequence represents an IgE heavy chain amino acid sequence, which is given in an example from the present invention Gape ö Length 421; 77.1%; Score 108; DB 6; Length 42 90.9%; Pred. No. 3.6e-08; ive 0; Mismatches 2; Indels 280 dydygcivbhebeekeivksir 301 2 GYGYQSIVDRPDFPKPIVRSIT 23 Conservative Local Similarity es 20; Conserv Sequence 421 AA; Query Match Matches ò 셤

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the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the DNA encoding the mouse IgE heavy chain C-C3-C4 domain with MIGIS virus used to create the epitopes used in the method of the invention
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                                                                                                                                                                                                                  Length 343;
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                                                                                                                                                                                                                                                                                                                                                                                                                            AAU80295 standard; protein; 343 AA
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                                                                                                                                                                                               Query Match
Best Local Similarity 90.97
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                                                                                                                                                                         Sequence 343 AA;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing cytotoxic T lymphocytes for treating e.g. autoimmune diseases, comprises culturing CD8+ T cells with antigen presenting cells to activate precursor CD8+ T cells specific for T the cell epitopes.
                                                                                                                                                                                                                                                                                                                                                                                       Cytotoxic T lymphocyte, CTL, tumour, antigen presenting cell, allergy, lupus, autoimmune disease, rheumatoid arthritis, autoimmune nephritis, psoriasis, APC, multiple sclerosis, autoimmune thyroiditis, hay fever, inflammatory bowel disease, insulin dependent diabetes, cell therapy, crohn's disease, allergic rhintis, graft versus host disease, aethma, transplant rejection, mouse, immunoglobulin E, 1gE.
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                                 Length 343;
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                             77.1%; Score 108; DB 5; Length 34 90.9%; Pred. No. 2.8e-08; ive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                     Mouse immunoglobulin E (IgE) a allelic protein.
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                                                                                                                                   191 GYGYQCIVDHPDFPKPIVRSIT 212
                                                                                                                                                                                                                                         AAE35111 standard; protein; 388 AA
                                                                                                         2 GYGYOSIVDRPDFPKPIVRSIT 23
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                             Query Match
Best Local Similarity 90.9'
Matches 20; Conservative
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Matches 20; Conserv
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Sequence 343 AA;
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This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCS) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and retainment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatities. The present sequence represents the mouse IgE heavy chain C2-C3-C4 domain optimised for an E.Coli expression system used to create the epitopes used in the method of the invention
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                                                 Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.
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                                                                                                                         Disclosure; Page 144-145; 151pp; English
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15-SEP-2000; 2000US-0232831P.
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nes 20; Conserv
WPI; 2002-383033
N-PSDB; ABK51142
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 332 AA;
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Synthetic.
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      This invention relates to a novel method for inducing an immune response against autologus immunoglobulin B (IgB) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCS) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating autologous IgE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermattiis. The present sequence represents the mouse IgE heavy chain C2-C3-C4 domain with the MIGIS fragment used to create the epitopes used in the method of the invention
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90.9%; Pred. No. 2.7e-08;
tive 0; Mismatches 2; Indels
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15-SEP-2000; 2000US-0232831P.
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Best Local Similarity 90.9
Matches 20; Conservative
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N-PSDB; ABK51140.
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Synthetic.
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Wang CY,

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This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (ISE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IGB, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen cell epitope (TH epitope) which is foreign to the animal, by antigen the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IGE in an animal. Which is useful for downregulating autologous IGE in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, as anathma and atopic dermatitis. The present sequence represents he mouse IGE heavy chain C2-C3-C4 domain optimised for a mammalian expression system used to create the epitopes used in the method of the invention
                                                                                                                                                                                                                                                   Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.
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                                                                                                                             Gautam A;
                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 140-141; 151pp; English.
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15-SEP-2000; 2000US-0232831P.
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06-SEP-2000; 2000DK-00001326.
15-SEP-2000; 2000US-0232831P.
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N-PSDB; ABK51141.
                                                                            (PHAR-) PHARMEXA AS
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                                                                                                                             Klysner S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antiganic peptides (I). (T) have anti-allergic, anti-anaphylactic and antiganic peptides (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of 1g5, and so a target effector site on the epsilon-heavy chain of 1g5, and so a target effector site on the epsilon-heavy chain of 1g5, and so a target effector site on the epsilon of mast calls and basophils and downrequiation of 1g5 synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against 1g5-mediated allergies, e.g. food allergies, asthma, maphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (nonmathylactogenic) antibodies. AAY9994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                   New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes immunoglobulin E (IgE)-CH3 domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 80.7%; Score 113; DB 3; Length 31 Best Local Similarity 95.5%; Pred. No. 4.3e-09; Matches 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 66-68; 155pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU80298 standard; protein; 332 AA.
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                                                                                                                                                                                                                                (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-SEP-2001; 2001WO-DK000579
                                                                                                                             99WO-US013959.
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                                                                                                                                                                                                                                                                                    Walfield AM;
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RESULT 4 AAE35112

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The present invention describes a transgenic, non-human animal with its genome altered to constitutively express a molecule having a constant region which can bind an IgE receptor on mast cells in the animals, the molecule having an immunoglobulin structure and being further capable of specifically binding a predetermined antigen. The transgenic animal is ubstances i.e. with antiallargic activity, to affect any allergic substances i.e. with antiallargic activity, to affect any allergic animal, and applying the substance to be evaluated. The present sequence is the mouse immunoglobulin E (IgE) heavy chain, given in the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-achimatic; asthma; anaphylactic; anti-achimatic; asthma; anaphylactic; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 82.9%; Score 116; DB 2; Length 56 Similarity 91.3%; Pred. No. 2.8e-09; 21; Conservative 1; Mismatches 1; Indels
                                                                                             Mouse; immunoglobulin E; IgE; allergy; transgenic animal.
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                                                                                                                                                                                                                                                                 20. .561
/label= immunoglobulin_E_heavy_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taya C, Matsuoka K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOKM-) TOKYO METROPOLITAN INST MEDICAL SCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic non-human animal allergy models.
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                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; Page 24-27; 42pp; English.
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                                              Mouse immunoglobulin E heavy chain.
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26-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method of producing cytotoxic T lymphocytes (CTLs) specific for one or more non-tumour self antigen T cell epitopes. The method involves loading antigen presenting cells (APCS) having class I major histocompatibility complex molecules with the T cell epitopes. The major histocompatibility complex molecules with the T cell epitopes. The invention is useful for the T cells specific for the T cells with the APCS to activate precursor CD8+T cells specific for the T cell epitopes. The invention is useful for treating autoimmune disease including rheumatoid arthritis, psoriasis, insulin dependent diabetes, crohn's disease, inflammatory bowel disease, graft versus host disease and transplant rejection and/or allergic disease such as food allergy, hay fever, allergic rhinitis, allergic asthma and venom allergy. The invention is also useful in cell therapy. The present sequence is mouse immunoglobulin E (IgB) b allelic protein. This protein is used in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing cytotoxic T lymphocytes for treating e.g. autoimmune diseases, comprises culturing CD8+ T cells with antigen presenting cells to activate precursor CD8+ T cells specific for T the cell epitopes.
                                                                                                                                                                                                                                                                                      Cytotoxic I lymphocyte; CTL; tumour; antigen presenting cell; allergy; lupus; autoimmune disease; rheumatoid arthritis; autoimmune nephritis; psoriasis; APC; multiple sclerosis; autoimmune thyroiditis; hay fever; inflammatory bowel disease; insulin dependent diabetes; cell therapy; Crohn's disease; allergic rhinitis; graft versus host disease; asthma; transplant rejection; mouse; immunoglobulin E; IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 O; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peterson PA, Shi W, Kong Y, Degraw J;
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                                                                                                                                                                                                                                          Mouse immunoglobulin E (IgE) b allelic protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               281 GYGYQCVVDRPDFPKPIVRSITL 303
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                                                                                           AAE35112 standard; protein; 423 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ORTH ) ORTHO-MCNEIL PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-2001; 2001US-0291300P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-MAY-2002; 2002WO-US015341.
                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-120673/11.
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The present invention describes immunoglobulin B (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (nonmachine) antibodies. AAY30994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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to
(functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epitope;
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Best Local Similarity 100.º
Marches 25; Conservative
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                                                                                                                                                                                                                                                           Sequence 25 AA;
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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic paptides (1). (1) have anti-allergic, anti-anaphylactic and antigenic paptides (1). (1) have anti-allergic, anti-anaphylactic and antigenic paptides (1). (1) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (1) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (1) that include a promiseuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (nonanaphylaxies) antibodies. AAYY9994 to AAX80084 represent amino acid anaphylactogenic) antibodies. AAYY9994 to AAX80084 represent amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
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                                     2; Indels
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92.1%; Score 129; DB 3;
92.0%; Pred. No. 1.6e-12;
                                                                                                                                                                                                                                                                                                          IgE immunogenic peptide conjugate SEQ ID NO:24.
                                   0; Mismatches
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                                                                        1 CGYGYQSIVDRPDFPKPIVRSITLC
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                                                                                                                                                                                                  AAY80017 standard; peptide; 46
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Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 26, 2004, 08:16:50 ; Search time 46.6 Seconds on:

Run

(without alignments) 151.581 Million cell updates/sec

US-09-701-623C-8 Title: Perfect score:

140 1 CGYGYQSIVDRPDFPKPIVRSITLC Sequence:

Scoring table:

25

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 segs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* geneseqp2000s:*geneseqp2001s:* geneseqp1980s:* geneseqp1990s:* geneseqp2002s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

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SUMMAKIES	. ai	AAYBOOO1	AAY80018	AAY80017	AAE35112	AAY17415	AAY79997	AAU80298	AAU80299	AAU80297	AAU80296	AAU80295	AAE35111	AAU80300	ABP96586	AAE35016	AAU80294	AAY80000	ABG74776	AAY79996	AAB03643	AAB06206	ABG74785	ABP96589	AAY80077	AAY79999
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## ALIGNMENTS

Immunoglobulin B; 1gB; epsilon heavy chain; antigenic; antigen; immunoglopenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy; disease; immunisation; anti-allergic; anti-anaphylactic; athmatic; asthma; anaphylaxis; dermatitis. Optimised IgE-CH3 domain antigen peptide for mouse IgE. AAY80001 standard; peptide; 25 AA (first entry) 15-MAY-2000 AAY80001; RESULT 1 

Mus sp. Synthetic.

W09967293-A1.

29-DEC-1999.

21-JUN-1999;

98US-00100287. 20-JUN-1998; (UNBI-) UNITED BIOMEDICAL INC.

Walfield AM; Wang CY,

WPI; 2000-160578/14.

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.

Claim 1; Page 100; 155pp; English.

for The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (1). (1) have anti-allergic, anti-anaphylactic and anti-gasthmatic properties. (1) induces polyclonal antibodies specific is a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downrequiation of IgE synthesis. Conjugates, or fusion peptides, containing (1) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (1) that include a promiscuous T helper cell epitope

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                                                                                                                                                                                                                                                                    01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OCT-2002 (TrEMBLrel. 18, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
MLD0627.
MLD0627.
Rhizobium loti (Mesorhizobium loti).
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales, Phyllobacteriaceae; Mesorhizobium.
NCBL_TaxID=381;
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Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium
NCBI_TaxID=36329;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical protein.
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TIGRFAMs; TIGR00360; ComEC_N-term; 1.
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STRAIN-MAFF303099;
MEDLINE=21082930; PubMed=11214968;
                                          47 CGYGYLGLILMPLLPK 62
1 CGYGYQSIVDRPDFPK 16
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SEQUENCE FROM N.A.
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SEQUENCE 753 AA:
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Seeger K., Sharp S., Smith R., Squares R., Squares S., Stevens laylor K., Tivey A., Unwin L., Whitehead S., Woodward J., Sulston J.E., Craig A., Newbold C., Barrell B.G. B., Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13.";
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Pred. No. 1.1e+02;
2; Mismatches 2; Indels
                                                                                                     Nature 419:527-531(2002).
EMBL, AL031745. CAD49017.1; -.
Hypothetical protein.
SEQUENCE 832 AA; 99310 MW; 3E4C1249C9FD459B CRC64;
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Best Local Similarity 66.7%;
Matches 8; Conservative 7
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28X227

177 COYGYULADDNRSCTVECSNHVFTERQGELSSPDFPRPYPRAL 219

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EDUDENCE FROM N.A.

BEDUENCE FROM N.A.

BENGO Y., Nonaka M., Saiga H., Kakinuma Y., Takahashi M.,

Marsushite M., Fujita T.,

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
Petromyzontiformes; Petromyzontidae; Lethenteron.
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Pred. No. 83;
4; Mismatches 7; Indels 21;
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                                                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
1-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last amnotation update)
Mannose-binding lectin-associated serine protease.
                                                722 AA
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InterPro; IPR001881; EGF Ca.
InterPro; IPR001254; PGF Like.
InterPro; IPR001314; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR00436; Sushi_SCR_CCP.
Fam; PP00431; CUB; 2.
Pfam; PP00084; sushi; 2.
Pfam; PP00089; trypsin; 1.
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SWART; SW00179; EGF CA; 1.
SWART; SW001020; TryD SPC; 1.
PROSITE; PS00110; ASX HYDROXYL; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01187; EGF CA; 1.
PROSITE; PS01047; EGF CA; 1.
PROSITE; PS01047; EGF CA; 1.
                                                PRT;
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SMART; SM00032; CCP; 2.
SMART; SM00042; CUB; 2.
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Best Local Similarity 25.6%;
Matches 11; Conservative
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                                                PRELIMINARY;
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                                                Q8AM90
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RESULT 11
                        Q8AW90
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Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
Nelson K.B., Tettelin H., Fouts D.E., Elsen J.A., Gill S.R.,
Noltzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
Nelson W.C., Peterson J.D., Popp M., Khouri H.M., Radune D.H.,
Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
Berry K.J., Plaut R.D., Wolf A.M., Warkins K.L., Nierman W.C.,
Thomason B., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
Frager C.M.;
                                                                                                             Cryptococcus neoformans var. neoformans.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Janbon G., Himmelreich U., Moyrand F., Improvisi L., Dromer F.;
"Casip is a membrane protein necessary for the O-acetylation of the
                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=198094;
                                                                                                                                                                                                                                                                                                                                               960 AA; 107503 MW; 6AA05D5FCD2650F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                Cryptococcus neoformans capsular polysaccharide.", Mol. Microblol. 42:453-467 (2001).
EMBL, ASSSES92, AAL35099.1, -.
GO, GO:0016740, F:transferase activity, IEA.
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34.6%; Score 48.5; DB 3;
Best Local Similarity 41.4%; Pred. No. 1.1e+02;
Matches 12; Conservative 4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 16;
Pred. No. 38;
2; Mismatches 6.
960 AA
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                                 Created)
PRT;
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EMBL; AE017030; AAP26057.1; -.
TIGR; BA2178; -.
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ilarity 50.0%;
Conservative
                                 20°,
                 ul-WAR-2002 (TrEMBLrel. 2: 01-MAR-2002 (TrEMBLrel. 2: 01-UTN-2003 (TrEMBLrel. 24 O-acetyltransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein.
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                  NCBI_TaxID=40410;
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Q8X227
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Q9PSZ5
Q9PSZ5;
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RAMEDRINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta; Pterygota,
Neoptera, Endopterygota, Diptera; Brachycera; Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                          Indels
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                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                   PRT; 1449 AA
  ed. No. 40;
Mismatches
     Pred. No.
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InterPro; IPR004010; Cache.
InterPro; IPR002035; VWF_A.
Best Local Similarity 35.3%; Pr
Matches 6; Conservative 7;
                                                                                                         117 EAVAQRPDLPEPLLRQL 133
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                                                                       6 OSIVDRPDFPKPIVRSI 22
                                                                                                                                                                                                                                                PRELIMINARY;
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SMART; SM00327; VWA; 1.
PROSITE; PS50234; VWFA;
SEQUENCE 1449 AA; 162
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09V917
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Endo Y., Takahashi M., Nakao M., Saiga H., Sekine H., Matsushita M.,
Nonaka M., Fujita T.;
Nonaka M., Fujita T.;
Two lineages of the serine protease
(MASP) in vertebrates ";
J. Immunol. 161:4924-4930(1998).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
-!- SIMILARITY: CENUNAINS 2 CUB DOMAINS.
EMBL; AB009075; BA868681; --
HSSP; PO0763; 1DPO.
                                                                        Gaps
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R SWART; SW00032; CCP; 2.

R SWART; SW0019; EGP_CA; 1.

R SWART; SW00100; ASX_HYDROXYL; 1.

R PROSITE; PS01180; CUB; 2.

R PROSITE; PS01180; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS01187; EGF_CA; 1.

R PROSITE; PS010135; TRYPSIN DOM; 1.

R PROSITE; PS010135; TRYPSIN_ER; 1.

R PROSITE; PS010135; TRYPSIN_ER; 1.

R PGF_Like domain; Hydrolase; Lectin; Protease; Serine protease.

SEQUENCE 722 AA; 79591 MW; 81DFB4F78F540B20 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Mannose-binding lectin-associated serine protease.
Lampetra japonica (Japanese lamprey) (Entrosphenus japonicus).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia; petromyzontiformes; Petromyzontidae; Lethenteron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
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Score 49; DB 5; Length 1449;
Pred. No. 1.46+02;
6; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO: GO: 0005509; F: calcium ion binding; IEA.
GO: GO: 0004263; F: calcium ion binding; IEA.
GO: GO: 0004263; F: chymotrypsin activity; IEA.
GO: GO: 0005529; F: peptidase activity; IEA.
GO: GO: 0004255; F: trypsin activity; IEA.
GO: GO: 0004255; F: trypsin activity; IEA.
GO: GO: 0004255; F: protecophilic cell adhesion; IEA.
GO: GO: 0006509; P: protecophilic cell adhesion; IEA.
InterPro; IPR000152; Asx hydroxyl_S.
InterPro; IPR00055; CUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 34.6%; Score 48.5; DB 13; Best Local Similarity 25.6%; Pred. No. 83; Matches 11; Conservative 4; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                         722 AA
                                                                                                                                                                                             609 GLGYAFLLDRSTGNTLAHPAFPRPLIORET 638
                                                                                                                                 --- PDFPKPIVRSIT 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR009003; Cys Ser_trypsin.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR00209; EGF_Ike.
InterPro; IPR001254; Peptidase_S1.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001314; Peptidase_S1A.
InterPro; IPR001436; Sushi_SCR_CCP.
                                                                                                                                                                                                                                                                                                                                                         PRT;
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PRINTS; PR00722; CHYMOTRYPSIN.
      35.0%;
         Query Match
Best Local Similarity 33.3
Matches 10; Conservative
                                                                                                                                 2 GYGYQSIVDR-----
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Pfam; PF00084; sushi; 2.
                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
STRAINER! / ATC 1339 / DSM 20539 / NCIB 9279;
MEDLINE=20036896; PubMed=10567266;
MEDLINE=20036896; PubMed=10567266;
Monite O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffar K.S., Qin H., Jiang L., Pamphille W., Crosby M., Shen M., Wanathevan J.J., Lam P., McDonald L., Uterback T., Zalewski C., Wanathevan J.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D., Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                               MEDLINE=21595285; PubMed=11759840; Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Sugimoto S., Sugimoto M., Takazawa M., Yamada M., Dabata S., Sugimoto S., Sugimoto M., Takazawa M., Yamada M., Babata S., Sugimoto S., Sugimoto M., Takazawa M., Yamada M., Babata S., Sugimoto S., Sugimoto S., Sugimoto M., Takazawa M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M., Yamada M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35.0%; Score 49; DB 16; Length 232; 43.8%; Pred. No. 21; tive 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria, Deinococcus-Thermus, Deinococci; Deinococcales, Deinococcasea, Deinococcus.
NCBL_TaxID=1299;
        Bacteria; Cyanobatteria; Nostocales; Nostocaceae; Nostoc.
NCBL_TaxID=103690;
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PROSTIE, PS00215; MITGCH CARRIER; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 433 AA; 46392 MW; 9089C90957FE4465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                         GO; GO:0046821; C:extrachromosomal DNA; IEA.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 232 AA; 26789 MW; 2DF174D14131DE14 CRC64;
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GO; GO:0005743; C:mitochondrial inner membrane; IBA.
GO; GO:0005818; F:binding; IBA.
GO; GO:0006810; P:transport; IBA.
InterPro; IPR004893; ARM.
InterPro; IPR004893; IRV.
InterPro; IPR004893; Mitoch carrier.
InterPro; IPR004891; Unk DeInSyn.
PF01816; LRV; 13.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein DR1773.
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EMBL; AE002019; AAF11328.1; -.
PIR; C75354; C75354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S YOSIVDRPDFPKPIVR 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 43.0.
Best Local 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Plasmid pcc7120alpha.
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                    SEQUENCE FROM N.A.

CA TRAINECTOR. Nipponbare;

A sasaki T., Matsumoto T., Yamamoto K.;

Sasaki T., Matsumoto T., Yamamoto K.;

A "Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC annet a consensual sativa (japonica cultivar-group) genomic DNA, chromosome 1, BAC ENDEL, AP00333; BAB91845.1; -.

DR GO GO:000333; BAB91845.1; -.

DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.

DR GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.

DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.

DR GO; GO:0005279; P:amino acid-polyamine transporter activity; IEA.

DR GO; GO:0005865; P:amino acid transport, IEA.

DR HIGEPEO; IPR002422; AA/rel_permease2.

DR InterPeo; IPR003006; Ig_MHC.

DR PEDM: PF01499; Aa_trans; 1.

DR PROSITE; PS00290; IGG MHC; I.

PROSITE; PS00290; IGG MHC; I.

CROTTENCE 443 AA; 47387 MW; 01EA6F36CDF22BBB CRC64;
                                                                                                              BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.4%; Score 49.5; DB 10; Length 443; Best Local Similarity 41.4%; Pred. No. 34; Matches 12; Conservative 4; Mismatches 8; Indels 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein; Plasmid.
SEQUENCE 165 AA; 19189 MW; 22E6A92532874A80 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNM-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein Alr7383.
ALR7983.
Anabaena sp. (strain PCC 7120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
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NCBI_TaxID=84600;
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RESULT 6
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RESULT 7.
28 YKB8
ID Q8 YKB
AC Q8 YKB
DT 01-MA
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Gaps
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ebrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Watch Match 35.7%; Score 50; DB 5; Length 338; Local Similarity 44.4%; Pred. No. 21; respective 3; Mismatches 7: Tradalm
                                                                                                                                                                                                                                                                             Length 164;
                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              investigating biology.";
Science 282:2012-2018 (1998).
EMBL: 298977; CAD56615.1; -..
WormPep; Y6942.14; CE32542.
InterPro; IPR001869; Collagen.
InterPro; IPR001869; Collagen.
Pfam; PF01391; Collagen; 3.
Pfam; PF01484; Collagen; 3.
Pfam; PF01484; Collagen; 3.
Pfam; PF01484; Collagen; 3.
                                                                                                                                                                                                        164 AA; 18687 MW; A3BD701D82D0A700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                      35.7%; Score 50; DB 2; 38.1%; Pred. No. 9.9; iive 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338 AA
GO, GO:0016787; F:hydrolase activity; IEA.
GO; GO:0009231; P:viramin E2 biosynthesis;
Interpro; IPR00925; GTP_cyclohydroII.
Fran; PF00925; GTP_cyclohydro2; 1.
Hydrolase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 YAIIIENPDYSNPIIRIHSSC 23
                                                                                                                                                                                                                                                                                                                                                                                                                 S YOSIVDRPDFPKPIVRSITLC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                              Best Local Similarity 38.1
Matches 8; Conservative
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B1103C09.36.
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SEQUENCE
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MEDLINE-21893127; PubMed=11895979;
MEDLINE-21893127; PubMed=11895979;
Ohashi N., Zhi N., Lin Q., Rikihisa Y.;
"Characterization and Transcriptional Analysis of Gene Clusters for a Type IV Secretion Machinery in Human Granulocytic and Monocytic Ehrlichiosis Agents.";
Enrichiosis Agents.";
Engl. AR392617; AAM00412.1;
GO; GO:0003935; F:GTP cyclohydrolase II activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Anaplasmataceae; Ehrlichia.
                                                                            DB 10; Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cytochrome c oxidase subunit IV.
Urechis caupo (Innkeeper worm) (Spoonworm).
Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
NCBI_TaxID=6431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36.8%; Score 51.5; DB 5; Length 186; illarity 45.5%; Pred. No. 6.6; Conservative 3; Mismatches 6; Indels 3
                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosenthal E.;
Submitted (UTN-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U30469, AAA74396.1;
GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
GO; GO:0006118; P:electron transport; IEA.
InterPro; IFR004203; COX4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02936; COX4; 1.
SEQUENCE 186 AA; 21084 MW; CC8EC1FASF84D766 CRC64;
          460 AA; 49420 MW; 549DD3183A0408B6 CRC64;
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01-UTN-2002 (TrEMBLrel. 21, Last sequence update)
01-UTN-2003 (TrEMBLrel. 24, Last annotation update)
GTP cyclohydrolase II (Fragment).
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                                                                            Query Match 37.5%; Score 52.5; 1
Best Local Similarity 37.9%; Pred. No. 12;
Matches 11; Conservative 6; Mismatches
                                                                                                                                                                                                                                                       266 GHGVFPTVYSSMNSKXDFPKVLLISLVLC 294
                                                                                                                                                                                                               2 GYG----YQSIVDRPDFPKPIVRSITLC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94155469; PubMed=8111976;
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les 10, Conserv
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          SEQUENCE
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Title: Perfect score:

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77x181 oryza sativ

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77x478 bordetella

77x473 bordetella

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77x473 bordetella

77x26 beet yellow

792x12 yersina pe

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Q8zyy6 salmonella
Q7xyk1 chlorarachn
pisum sativ
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
001/2002.23 Drotein (P0700All.4 protein).
07/22 sativa (Rice), and oryza sativa (japonica cultivar-group).
07/22 sativa (japonica cultivar-group).
Spermatophyta, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE TO NIPPOIDER: Sasaki T., Matsumoto T., Yamamoto K.; Sasaki T., Matsumoto T., Yamamoto K.; Clorya sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC Clore:P0712E02., Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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Q8KX54
Q8ZT42
Q8EIZ2
                                 Q7W4Q2
Q7VU73
Q7VU73
Q7VU73
Q65856
Q92UW6
Q92UW6
Q97YZF1
Q7YZF1
Q7YZF0
Q97YZF0
Q97YZF0
Q97YZF0
Q97YZF0
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Q8Z996
Q7XYK1
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Q88DM6
O69727
Q7TVR2
Q94259
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   PRELIMINARY;
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Q94D33
   Q27123 urechis cau
Q87pm4 ehrlichia c
Q84c0 caenorhabdi
Q84gu5 oryza sativ
O97701 sulfolobus
Q87kb8 anabaena sp
Q87kb1 deinococcus
Q9717 drosophila
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Q81r78 bacillus an
Q98md1 rhizobium 1
Q8i283 plasmodium
Q91925 xenopus lae
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Q8aw90 lampetra ja
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                                                                               February 26, 2004, 08:18:11; Search time 31.4 Seconds (without alignments) 251.209 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 CGYGYQSIVDRPDFPKPIVRSITLC
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Maximum Match 100%
Listing first 45 summaries
                                                              using sw model
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QBRPM4
QBRPM4
QBLQU5
QBYKB8
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QBYYJ1
Q9V917
Q9V917
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Match Length DB
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Score

Result

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Job time : 8.4 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                             MEDLINE=21595285; PubMed=11759840;

Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,

Ratanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,

Rishida Y., Kohara M., Matsumoto M., Muraki A.,

Rishida Y., Kohara M., Matsumoto M., Muraki A.,

Rishida Y., Kohara M., Matsumoto M., Muraki A.,

Radada M., Tabata S.,

Sugimoto M., Takazawa M., Yamada M.,

Yamada M., Tabata S.,

Tomplere genomic sequence of the filamentous nitrogen-fixing

Transpacterium Anabaena sp. strain PCC 7120.";

DNA Res. 81205-213(2001).

Thyrrion: Catalyzes a salvage reaction resulting in the formation

of AMP, that is energically less costly than de novo synthesis.

C. - CATALYTY CATIVITY: AMP + diphosphate = adenine + 5-phospho-

C. - PATRWAY: Purine salvage.

C. - PATRWAY: Purine salvage.

C. - SIDBUNT: Homodimer (By similarity).

C. - SIDBUNT: Belongs to the purine/pyrimidine

Dhosphoribosyltransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lytechinus pictus (Painted sea urchin).
Bukaryota, Metazoa, Echinodermata, Eleutherozoa, Echinozoa,
Echinoidea, Euechinoidea, Echinacea, Temnopleuroida, Toxopneustidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGRFAMS; TIGR01090; apt; 1.
PROSITE; PS00103; PUR PYR PR TRANSFER; 1.
Transferase; Glycosyltransferase; Purine salvage; Complete proteome.
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Pred. No. 7.9;
                        Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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InterPro; IPR005764; Ade phspho_trans.
InterPro; IPR00275; Pr/py_rp_transf.
InterPro; IPR000836; PRTransferase.
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il Similarity 61.1%;
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Matches 11; Conserv
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Q25378;
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KPC1 LYTPI
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    similarity).
    -!- SIMILARITY: Contains 2 zinc-dependent phorbol-ester and DAG binding domains.
    -!- SIMILARITY: Contains 1 C2 domain.
    -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. PKC
    -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases.

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                                                                                                                                                                  as
(By
sea urchin Lytechinus pictus.";
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This is a calcium-activated, phospholipid-dependent,
serine- and threonine-specific enzyme (By similarity).
-!- FUNCTION: PCC is activated by diacylglycerol which in turn
phosphorylates a range of cellular proteins. PCC also serves as
the receptor for phorbol esters, a class of tumor promoters (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
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R HSSP, POGESO, 1TEN.

R INTERPRO; IPRO00008; C2.

R INTERPRO; IPRO000913; C2.

R INTERPRO; IPRO000913; C2.

R INTERPRO; IPRO000913; C2.

R INTERPRO; IPRO00091; PATABAS C.

R INTERPRO; IPRO00091; PATABAS C.

R INTERPRO; IPRO0019; PATABAS C.

R INTERPRO; IPRO0129; PATABAS C.

R PÉAM; PF00186; C2.

R PÉAM; PF00180; DAG PE-bind; 2.

R PÉAM; PF00180; DAG PE-bind; 2.

R PRINTS; PR00109; TYTKLNASE C; 1.

R PRINTS; PR00109; TYTKLNASE C; 1.

R PRANTS; SW00109; TYTKLNASE C.

R SMART; SW00109; TYTKLNASE C.

R SMART; SW00109; C2. DOMAIN.

R PROSITE; PS00049; C2. DOMAIN.

R PROSITE; PS00049; C2. DOMAIN.

R PROSITE; PS00049; DAG PE-BIND DOM.

R PROSITE; PS00049; DAG PE-BIND DOM.

R PROSITE; PS000107; PROTEIN KINASE ATP; 1.

R PROSITE; PS00117; PROTEIN KINASE ST; 1.

R PROSITE; PS00117; PROTEIN KINASE ST; 1.

R PROSITE; PS00117; PROTEIN KINASE ST; 1.

R PROSITE; PS00117; PROTEIN KINASE ST; 1.

R PROSITE; PS00114; PROTEIN KINASE ST; 1.

R PROSITE; PS00114; PROTEIN KINASE ST; 1.

R PROSITE; PS00114; PROTEIN KINASE ST; 1.

R PROSITE; PS00114; PROTEIN KINASE ST; 1.

R PROSITE; PS00114; PROTEIN KINASE ST; 1.

R PROSITE; PS00114; PROTEIN KINASE ST; 1.

R PROSITE; PS00114; PROTEIN KINASE ST; 1.
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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DOMAIN
28 77 PHORBOL-ESTER AND
NOMAIN 93 142 PHORBOL-ESTER AND
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Pred. No.
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74871 MW;
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Best Local Similarity 43.5%;
Matches 10; Conservative
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15-MAR-2004 (Rel. 43, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
NADH-quinone oxidoorductase chain 3 (EC 1.6.99.5) (NADH dehydrogenase il, chain G) (NDH-1, chain G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-21470413; PubMed=11586360;
MEDLINE=21470413; PubMed=11586360;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Fersinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=KINS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Pernan N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Paraley S.C., McDonough K.A., Nilles W.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                          Gaps
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Enterobacteriaceae, Yersinia.
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                                                                                                                                                                                                                                       Query Match
33.6%; Score 47; DB 1; Length 699;
Best Local Similarity 30.0%; Pred. No. 25;
Matches 6; Conservative 9; Mismatches 5; Indels
                     24 GTP (BY SIMILARITY).
92 GTP (BY SIMILARITY).
445 GTP (BY SIMILARITY).
77413 MW, EC17B5350DDCG311 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of Yersinia pestis KIM.";
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                    396 CNSDHKVILERMEFPEPVIQ 415
                                                                                                                                                                                                                                                                           1 CGYGYQSIVDRPDFPKPIVR 20
                 EMBL; AE016801; AA009792.1; -
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145
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR003031; Complex1 75K.
InterPro; IPR001041; Perredoxin.
InterPro; IPR001041; Perredoxin.
Pfam; PF00111; fer2; 1.
Pfam; PF00111; fer2; 1.
Pfam; PF00111; fer2; 1.
Pfam; PF00111; fer2; 1.
PROSITE; PS00641; COMPLEX1 75K 1; 1.
PROSITE; PS00642; COMPLEX1 75K 2; 1.
PROSITE; PS00643; COMPLEX1 75K 2; 1.
Oxidoreductase; NAD; Metal-Jahding; Iron; Iron-sulfur; 2Fe-2S; 4Fe-4S; Quinone; Ubiquinone; Complete proteome.
                                                                                      sulfur (Fe-S) centers, to quinones in the respiratory chain. The immediate electron acceptor for the enzyme in this species is believed to be ubiquinone. Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient (By similarity).

-!- CATALYTIC ACTIVITY: NDH + quinone = NAD(+) + quinol.
                                                                                                                                                                                                                                                                                                                                                                                                     (By similarity).
--- SUBDART: Composed of 13 different subunits. Subunits nuoCD, E, F, and G constitute the peripheral sector of the complex.
---- SIMILARITY: Belongs to the complex I 75 kDa subunit family.
J. Bacteriol. 184:4601-4611(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RON-SULFUR 1 (2FE-2S) (BY S; RON-SULFUR 1 (2FE-2S) (BY S; RON-SULFUR 1 (2FE-2S) (BY S; RON-SULFUR 2 (4FE-4S) (BY S; RON-SULFUR 2 (4FE-4S) (BY S; RON-SULFUR 2 (4FE-4S) (BY S; RON-SULFUR 3 (4FE-4S) (BY S; RON-SULFUR 3 (4FE-4S) (BY S; RON-SULFUR 3 (4FE-4S) (BY S; RON-SULFUR 4 (4FE-4S) (BY S; RON-SULFUR 4 (4FE-4S) (POTER 10 S) (POTER 2 (4FE-4S) (POTER 3 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4FE-4S) (POTER 4 (4
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08YNI3;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Adenine phosphoribosyltransferase (EC 2.4.2.7) (APRT).
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34 IRON-SULFUR 1
45 IRON-SULFUR 1
48 IRON-SULFUR 1
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AJ414152; CAC91352.1; -. EMBL; AE013767; AAM85204.1; -.
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Best Local Similarity 47.1.
Best Local Similarity
A7.1.
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NCBI_TaxID=672;
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EFG_VIBVU
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                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.cib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
Probable porphobilinogen deaminase (EC 2.5.1.61) (PBG) (Hydroxymethylbilane synthase) (HWBS) (Pre-uroporphyrinogen synthase).
HEMC OR CT299.
                                                                                                                                      Aravind L.,
                                                                                                                                                                      "Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis."; Science 282:754-75(1998).
-!- FUNCTION: Tetrapolymerization of the monopyrrole PBG into the hydroxymethylbilane preuroporphyrinogen in several discrete steps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                             (By similarity).
-!- CATALYTIC ACTIVITY: 4 porphobilinogen + H(2)O = hydroxymethylbilane + 4 NH(3).
-!- PATHWAY: Porphyrin biosynthesis by the C5 pathway; fourth step.
-!- SIMILARITY: Belongs to the HMBS family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21396508; PubMed=11481431;
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ..
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                                                                                                                      MEDLINE-99000809; PubMed-9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Ara
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin B.V.,
                                          Chlamydia trachomatis.
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.6%; Score 47; DB 1; Length 241; 47.8%; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR.2004 (Rel. 43, Created)
15-MAR.2004 (Rel. 43, Laxt sequence update)
15-MAR.2004 (Rel. 43, Laxt sequence update)
15-MAR.2004 (Rel. 43, Laxt annotation update)
Probable sulfoacetaldehyde acetyltransferase (BC 2.3.3.15)
RASC OR RABOSTO OR SMB21530
RABIOTOLI (Sinorhizobium meliloti)
Plasmid pSymB (megaplasmid 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD002745; Porphobil deam; 1.
PROSITE; PS00533; PORPHOBILINOGEN DEAM; FALSE NEG.
Porphyrin biosynthesis; Transferase; Complete proteome.
SEQUENCE 241 AA; 26996 MW; FR9FE00C20BF7044 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         591 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE001302, AAC67892.1; -.
PIR; EN1532, E71532.
HAKSP, PO6983, 1PDA.
HAMAP, MF 00260, atypical; 1.
InterPro; IFR000860; Porphobil deam.
PRIMTS, PR01379; Porphobil deam.
PRIMTS, PR0151; PORPHBDMNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 CDLGIHSAKDLPENPKATVVSIT 112
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Best Local Similarity 47.8%
Matches 11; Conservative
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                                                                                              FROM N.A.
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                                                                   NCBI_TaxID=813;
                                                                                                                                                               Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       XSC RHIME
                                                                                             SEQUENCE
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: This protein promotes the GPP-dependent translocation of
the nascent protein chain from the A-site to the P-site of the
Golding B., Puehler A.;
"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinorhizobium meliloti",
Proc. NaLl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
-!-CATALYTICA ACTIVITY: Acetyl phosphate + sulfite = 2-sulfoacetaldehyde + phosphate
-!-COFACTOR: Binds 1 magnesium ion and 1 thiamine pyrophosphate per subunit (By similarity).
-!-PATHMAX: Anaerobic taurine degradation; second step.
-!-PATHMAX: Anaerobic taurine degradation; second step.
-!-SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!-SIMILARITY: Belongs to the TPP enzyme family.
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-1- SIMILARITY: Belongs to the GTP-binding elongation factor family.
EF-G/EF-2 subfamily.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transferase; Flavoprotein; Thiamine pyrophosphate; Metal-binding; Magnesium; Complete proteome; Plasmid.
SEQUENCE 591 AA; 64157 MW; 7234D44FB221EB97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 1; Length 591;
Pred, No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Indels
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InterPro; IPRO00399; Pyruvate_decarb.
Pfam; PF00205: TPP enzymes; 1.
Pfam; PF02775; TPP_enzymes C; 1.
Pfam; PF02776; TPP_enzymes N; 1.
PROSITE; PS00187; TPP_ENZYMES; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       433 CGYGFPSÍVGAKIGCPDVP 451
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Best Local Similarity 52.6%;
Matches 10; Conservative 1
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SEQUENCE
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Matches
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                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-UUL-1989 (Rel. 11, Created)
01-UUL-1989 (Rel. 11, Last sequence update)
Cycurone coxidase subunit IV isoform 1, mitochondrial precursor (EC 1.9.3.1) (COX IV-1) (Cytochrome c oxidase subunit OX isoform 1, mitochondrial precursor (EC 1.9.3.1) (COX IV-1) (Cytochrome c oxidase polypeptide IV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRANTH-Wister; TISSUE-Liver;
MEDLINE-89296488; PubMed-2544659;
Gopalan G., Droste M., Kadenbach B.;
"Nucleotide sequence of cDNA encoding subunit IV of cytochrome coxidase from fetal rat liver.";
Nucleic Acids Res. 17:4376-4376(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goto Y., Amuro N., Okazaki T.;
"Nucleotide sequence of cDNA for rat brain and liver cytochrome
oxidase subunit IV.";
Nucleic Acids Res. 17:2851-2851(1989).
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Pred. No. 17;
                                                                                                                                                                                                                              HAWAP; ME 00054; - 1.

InterPro; IPR000495; BF GTPbind.
InterPro; IPR000649; BFG TIL.
InterPro; IPR000517; BFG III.
InterPro; IPR009121; BFG IV.
InterPro; IPR004161; BFTG IV.
InterPro; IPR009009; Translat_factor.
InterPro; IPR009009; Translat_factor.
Pfam; PF00679; BFG C; 1.
Pfam; PF000409; GTP EFTU; 1.
Pfam; PF00109; GTP EFTU; 1.
Pfam; PR00114; GTP EFTU; 1.
PR011F; PR00115; BF0CTOR GTP; 1.
PR05ITE; PR00115; BF0CTOR GTP; 1.
PR05ITE; PR00115; BF0CTOR GTP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17 24 GTP (BY SIMILARITY).
88 92 GTP (BY SIMILARITY).
142 145 GTP (BY SIMILARITY).
699 AA, 77589 MW, 1178A114F1AA87AC CRC64;
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MEDLINE-89240039; PubMed=2541414;
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                                                                                                                                                                                                            EMBL; AP005082; BAC61034.1; -.
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30.0%;
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EF-G/EF-2 subfamily
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Best Local Similarity
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NP_BIND
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -:- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)0.
-:- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
-:- SIMILARITY: Belongs to the cytochrome c oxidase IV family.
                                                                                                                                                                                                                                                                                                                                                                                                                           Virbasius J.V., Scarpulla R.C.; "The rat cytochrome c oxidase subunit IV gene family: tissue-specific and hormonal differences in subunit IV and cytochrome c mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schaegger H., Noack H., Halanek W., Brandt U., von Jagow G.; "Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequences suggest identity of the fetal heart and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                              MEDLINE=90326528; PubMed=2165254; Amuro N., Yamada M., Goto Y., Okazaki T.; (Complete nucleotide sequence of the gene encoding rat cytochrome coxidase subunit IV."; Nucleic Acids Res. 18:3992-3992(1990).
                                oxidase subunit IV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           adult liver isoform.";

Eur. J. Biochem. 230:235-241(1995).

-!- FUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome coxidase, the terminal oxidase in mitochondrial electron transport.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF02936; COX4; 1.
Oxidoreductase; Inner membrane; Mitochondrion; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AA; 19514 MW; F0187C76B7A1A9FE CRC64;
                                O
Yamada M., Amuro N., Goto Y., Okazaki T.; structural organization of the rat cytochrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic Acids Res. 18:6581-6586(1990).
                                                                                          . Biol. Chem. 265:7687-7692(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 YGYOSIVDRPDFPKPIVRSITL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 YALPSYVDRRDYPLPDVAHVKL 54
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91067442; PubMed=2174541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 23-32.
STRAIN=Wistar; TISSUE=Liver;
MEDLINE=95324529; PubMed=7601105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X14209; CAA32426.1; -.
EMBL; X15029; CAA33133.1; -.
EMBL; J05425; AAA40949.1; -.
EMBL; X54081; CAA38018.1; -.
PIR; A35209; A35209.
InterPro; IPR004203; COX4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 40, Created)
(Rel. 40, Last seq
(Rel. 43, Last anno
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                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                      [5]
SEQUENCE FROM
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16-OCT-2001 (
15-MAR-2004 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression.",
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us-09-701-623c-8.rsp

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[2]
SEQUENCE OF 1-39, AND CHARACTERIZATION.
                      MEDLINE=99173910; PubMed=10074080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vibrio parahaemolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=670;
                                                                                                                                                                                                                                                                                                                           TIGR; TM1130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFG_VIBPA
Q87<u>L</u>45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
EFG_VIBPA
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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMEL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                            STRAIN=MSSB / DSM 3109 / ATCC 43589;
MEDLINE=92587316; PubMed=10360571;
MEDLINE=92587316; PubMed=10360571;
MEJSON K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Prat, M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Rleischmann R.D., Eisen J.A., White O.,
Exipherg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
Nature 399:323-329(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                          CYTOCHROME C OXIDASE SUBUNIT IV ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                A -> R (IN REF. 1).
S -> N (IN REF. 1).
MQ -> IE (IN REF. 1; AAB02139 AND 2).
D30B1DBBE14FDBEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
15-WAY-2004 (Rel. 43, Last annotation update)
Phosphate acetyltransferase (EC 2.3.1.8) (Phosphotransacetylase)
PTA OR TM1130.
MEDLINE=91378465; PubMed=1654830;
Carter R.S., Avadhani N.G.;
"Cloning and characterization of the mouse cytochrome c oxidase
                                                                                                                                                                                                                                                                             PIR; S12142; S12142.
MGD; MGI:88473; Cox4il.
GG; GO:005739; C:mitcochondrion; IDA.
InterPro; IPR004203; COX4.
Pfam; PF02336; COX4; 1.
Oxidoreductase; Inner membrane; Mitochondrion; Transit peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     34.3%; Score 48; DB 1; Length 169; ilarity 36.4%; Pred. No. 3.8; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 AA
                                                                                                                                                                                                                                                                                                                                                 MITOCHONDRION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 YGYOSIVDRPDFPKPIVRSITL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 YAFPTYADRRDYPLPDVAHVTM 54
                                                                                                                                                                                                                                 EMBL, M37831, AAB02139.1; -.
BMBL, M3034, AAB02139.1; JOINED.
EMBL, M37829; AAB02140.1; -.
EMBL, X54691; CAA38507.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                     141 M
19530 MW;
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169 AA;
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tes 8; Conserv
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Q9XOL4;
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CONFLICT
CONFLICT
SEQUENCE
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Matches
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-: FUNCTION: This protein promotes the GTP-dependent translocation of the naccent protein chain from the A-site to the P-site of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: Belongs to the GTP-binding elongation factor family.
DOCK A.-K., Glasemacher J., Schmidt R., Schoenheit P.,
BOCK A.-K., Glasemacher J., Schmidt R., Schoenheit P.,
Purification and characterization of two extremely thermostable
arrymes, phosphate acetyltransferase and acetate Kinase, from the
hyperthermophilic eubacterium Thermotoga maritima.",
J. Bacteriol. 181:1861-1867(1999).
-!- FUNCTION: IN ADDITION TO ACETYL-COA (100%), THE ENZYME ACCEPTS
PROPIONYL-COA (60%) AND BUTNYYL-COA (30%). HAS A TEMPERATURE
OPTIMIN AT 90 DEGREES CELGIUS.
-!- CATALYTIC ACTIVITY: Acetyl-COA + phosphate = COA + acetyl
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0
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-:- SUBCELLIAR LOCATION: Cytoplasmic (Potential).
-:- SIMILARITY: BELONGS TO THE PHOSPHATE ACETYLTRANSFERASE AND BUTYRYLIRANSFERASE FAMILY. MORE SIMILAR TO PTB THAN PTA.
                                                                                                                                                                                                                                                                                                                                                                            phosphate.
-!- PATHWAY: Conversion of acetate to acety1-CoA; second step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 48; DB 1; Length 294;
Pred. No. 6.9;
6; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR002505; PTA_PTB.
Pfam: PF01515; PTA_PTB; 1.
Transferase; Acyltransferase; Complete proteome.
CONFLICT 11 R -> Y (IN REF. 2).
SEQUENCE 294 AA; 32093 MW; F4B98B3CAE120AFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Elongation factor G (EF-G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      699 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001770; AAD36206.1; -. PIR; G72293; G72293.
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Best Local Similarity 46.7%;
Matches 7; Conservative 6
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122 SVMEIPDFPRPLIIS 136
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Cytochrome c oxidase subunit IV isoform 1 (EC 1.9.3.1) (COX IV-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                               NON TER
SEQUENCE
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CX41_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                Feldmann H., Mannhaupt G., Vetter I.;
Submitted (MAR-1992) to the ENBL/GenBank/DDBJ databases.
-!- FUNCTION: Necessary for the structural stability of L-A double-
stranded RNA-containing particles. Necessary for growth at 37
degrees Celsius as well as for maintenance of the Killer plasmid.
-!- SIMILARITY: TO S.POMBE SPAC4G8.14C.
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
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                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=89131254; PubMed=3916862;
Tob-E A., Sahashi Y.;
"The PETIS locus of Saccharomyces cerevisiae: a complex locus containing multiple genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34.6%; Score 48.5; DB 1; Length 363; 55.0%; Pred. No. 7.2; ive 3; Mismatches 5; Indels 1
                         35.0%; Score 49; DB 1; Length 705; llarity 50.0%; Pred. No. 12; Conservative 2; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CFB358F8ACF6EA4C CRC64;
   77866 MW; 8D75A4AEEB102499 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO:0019048; P:virus-host interaction; IMP.
7LICT 15 15 1 -> 11 (IN REF. 1).
7LICT 82 82 MISSING (IN REF. 1).
                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 38, Created)
(Rel. 38, Last sequence update)
(Rel. 41, Last annotation update)
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                                                                                                                                                          PRT;
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                                                                         5 YOSIVDRPDFPKPIVRSI
                                                                                               513 YNEVYDRPVKPTPVVAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X59720; CAA42310.1; -.
                                                                                                                                                                                                                  MAK32 protein.
MAK32 OR YCR019W OR YCR19W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
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                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                               Yeast 1:159-171(1985)
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GermOnline; 138924;
     705 AA;
                                    Local Similarity
Les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 5
CX41 PITPI
ID CX41 PITPI
AC 04658;
DT 15-JUL-1999
DT 28-FEB-2003
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28-FEB-2003
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P23060;
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     SECUENCE
                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mitochondrial electron transport.
-!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome c + 2 H(2)0.
-!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
-!- SUBLEARITY: Belongs to the cytochrome c oxidase IV family.
                                                                                                                                                                                                                                                                                                                          MEDLINE=97277139; PubMed=9115172; Wu W. Goodman M., Lomax M.I., Grossman L.I.; Wu W., Goodman M., Lomax M.I., Grossman L.I.; Use vidence for "Molecular evolution of Cytochrome c oxidase subunit IV: evidence for positive selection in simian primates."; J. Mol. Bvol. 44:477-491(1997).

-!- PUNCTION: This protein is one of the nuclear-coded polypeptide chains of cytochrome c oxidase, the terminal oxidase in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEE-1991 (Rel. 17, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-OCT-1993 (Rel. 43, Last annotation update)
Cytochrome c oxidase subunit IV isoform 1, mitochondrial precursor (EC 1.9.3.1) (COX IV-1) (Cytochrome c oxidase polypeptide IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Platyrrhini, Cebidae, Pitheciinae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    144 AA; 16917 MW; 5573133B773E5C89 CRC64;
(Cytochrome c oxidase polypeptide IV) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF02936; COX4; 1.
Oxidoreductase; Inner membrane; Mitochondrion.
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                                                                         pithecia (White-faced saki)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AF042770; AAB97849.1; -.
EMBL; AF042768; AAB97849.1; JOINED.
EMBL; AF042769; AAB97849.1; JOINED.
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MEDLINE=91057158; PubMed=2173832;
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Best Local Similarity
Matches 10; Conserv
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=LOU/C/WSL;
PubMed=6292865;
Hellman L., Pettersson U., Engstroem A., Karlsson T., Bennich H.;
"Structure and evolution of the heavy chain from rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 205-306 FROM N.A.

MEDLINE=821/4576; PubMed=6803238;

Hellman L., Pettersson U., Bennich H.;

Hellman L., Pettersson U., Bennich H.;

("characterization and molecular cloning of the mRNA for the heavy ("epsilon) chain of rat immunoglobulin E.";

Proc. Natl. Acad. Sci. U.S.A. 79:1264-1268(1982).

-I- SIMILARITY: Contains 4 immunoglobulin-like domains.
                                                                                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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MEDLINE=83182019; PubMed=6820340;
Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.,
A clonde cDNa probe for rat immunoglobulin epsilon heavy chain:
construction, identification, and DNA sequence.";
DNA 1:335-343(1982).
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                                                                                                                                                                                                                                                                                                                                                                                              Length 421;
                                                                                                                                                                                                                                                                                                                                                                  CH4.

BY SIMILARITY.

N-LINKED (GLCNAC. ...) (POTENTINKED (GLCNAC. ...)
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21-JUL-1986 (Rel. 01, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
19 epsilon chain C region.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2)
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                                                                                                                                                                                                                                                                                                                                                  47320 MW;
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90.9%;
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InterPro; IPR007110; Ig-like
                                                                                                                                                                                                                                                                                                                                                                                                                                             20; Conservative
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       Query Match
Best Local Similarity
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HSSP; P01854; 110
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X REDLINE=2511545; PubMed=12622808;
A COben G.W. Blament D., Galperin M., Heilig R., Lecompte O., Coben G.W., Prieur D., Querellou U., Ripp R., Thierry J.-C.,
A Poch O., Prieur D., Querellou U., Ripp R., Thierry J.-C.,
A van der Oost J., Weissenbach J., Zivanovic Y., Forterre P.;
T. An integrated analysis of the genome of the hyperthermophilic archaeon Pyrococcus abyssi.",
Mol. Microbiol. 47:1495-1512(2003).
I. Mol. Microbiol. 47:1495-1512(2003).
I. C.: CATALYTIC ACTIVITY: ATP + N(2) - formyl-N(1) - (5-phospho-D-ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-(formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine + L-glutamate.
C. I- PATHWAX: De novo purine biosynthesis; fourth step.
I. SUBGNUT: Heterodimer of two subunits, purQ and purL.
C. I- SUBCINITAR LOCATION: Cytoplasmic (By similarity).
C. I- SIMILARITY: Belongs to the FGAMS family.
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last amnotation update)
Phosphoribosylformylglycinamidine synthase II (EC 6.3.5.3) (FGAM
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PIR, A75026; A75026.

IndamP, Mr. 00420; -; 1.

InterPro; IPR00728; AIR. synth.

Pfam; PF00586; AIRS; 2.

Pfam; PF07569; AIRS_C; 2.

Purine blosynthesis; Ligase; ATP-binding; Complete proteome.

NP_BIND
Score 85; DB 1; Length 429;
Pred. No. 2.2e-05;
0; Mismatches 5; Indels
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Best Local Similarity 77.39
Matches 17; Conservative
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Q9UXW6;
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A; Nore: the nucleotide sequence was submitted to the EMBL Data Library, July 1990
B; Schaegger, H.; Nacack, H.; Halands, W.; Brandt, U.; von Jagow, G.
By. Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term
A; Reference number: 865373
A; Reference number: 865373; MUID:95324529; PMID:7601105
A; Accession: 865373
A; Reference received: protein
A; Residues: 23-45 «SCH»
A; Accession: 25-1; 81/1; 125/1
C; Genetics:
C; Genetics:
A; Accession: 25-1; 81/1; 125/1
C; Function: 25-1; 81/1; 125/1
C; Function: the cytochrome-c oxidase complex catalyzes the oxidation of four molecule is from the mitochondrial matrix producing two molecules of water and lowering the conce A; Pathway: oxidative phosphorylation; respiratory chain
C; Superfamily: cytochrome-c oxidase chain IV
C; Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane
C; Superfamily: cytochrome-c oxidase chain IV
C; Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane
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F; 73-103/pomain: transmembrane helix #status predicted <TRO:
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A;Status: preliminary
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A;Cross-references: GB:U5425; NID:g203516; PIDN:AAA40949.1; PID:g203517
A;Cross-references: GB:U5425; NID:g203516; T.
Nucleic Acids Res. 18, 3992, 1990
Nucleic Acids Res. 18, 3992, 1990
A;Fille: Complete nucleotide sequence of the gene encoding rat cytochrome c oxidase subtactions S12724; MUD:90326528; PMID:2165254
A;Accession: S12724
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A;Residues 1.169 cAMU.
A;Cross references: EMBL:J05425; NID:g203516; PIDN:AA40949.1; PID:g203517
B;Goto, Y.; Amuro, N.; Okazaki, T.
Rucialc Adids Res. 17, 2851, 199
A;Title: Nuclectide sequence of cDNA for rat brain and liver cytochrome c oxidase subun:
A;Reference number: S04070; MUID:89240039; PMID:2541414
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A; Residues: 1-150 <COP-

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A; Cross-references: EMBL:X15029; NID:955980; PIDN:CAA33133.1; PID:955981

R; Virbasius, J.V.; Scarpulla, R.C.

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Proc. Natl. Acad. Sci. U.S.A. 92, 7177-7181, 1995
A;Title: A chloroplast processing enzyme involved in precursor maturation shares a zinc-
A;Reference number: Z15733; MUID:95365331; PMID:7638164
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Nucleic Acids Res. 17, 4376, 1989
Nucleic Acids Res. 17, 4376, 1989
A; Title: Nucleotide sequence of cDNA encoding subunit IV of cytochrome c oxidase from
A; Reference number: S04593; MUID:89294488; PMID:2544859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytochrome-c oxidase (EC 1.9.3.1) chain IV precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Aug-1990 #sequence revision 10-Aug-1990 #text change 11-Jun-1999
C;Date: 10-Aug-1990; S1274; S046070; S04593; S14190; S65573
R;Yamada, M.; Amuro, N.; Goto, Y.; Okazaki, T.
J. Biol. Chem. 265, 768-7692, 1990
A;Title: Structural organization of the rat cytochrome c oxidase subunit IV gene.
A;Reference number: A35209; MUID:90237079; PMID:21S9010
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pitrilysin (EC 3.4.24.55) - garden pea
C;Species: Pisum sativum (garden pea)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: T06521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: T06521
A,Status: translated from GB/EMBL/DDBJ
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-1259 <VANA
A,Residues: 1-1259 <VANA
C,COSS-references: EMBL:UZ5111; NID:g1065907; PIDN:AAA81472.1; PID:g799369
C,Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

34.3%; Score 48; DB

Best Local Similarity 38.1%; Pred. No. 68;

Matches 8; Conservative 5; Mismatches
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                                                                                                                                                                                       Silving Number oxidase (EC 1.9.3.1) chain IV precursor - mouse Cytochrome-c oxidase (EC 1.9.3.1) chain IV precursor - mouse Cytochrome oxidase (BC 1.9.3.1) chain IV precursor - mouse CySpecies: Mus musculus (house mouse)
CySpecies: Number 1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CyAccession: S12142; S16114
RyGroseman, L. 1; Akamatau, M.
Nucleic Acids Res. 18, 6454, 1990
A;Title: Nucleotide sequence of a mouse cDNA for subunit IV of cytochrome c oxidase.
A;Accession: S12142
A;Accession: S12142
A;Kesidues: 1-169 ocRO.
A;Cross-references: BMBL:X54691; NID:950518; PIDN:CAA38507.1; PID:950519
A;Esperimental source: strain Balb/c
R;Carter; R.S.; Avadhani N.G
Arch: Biochem: Biochem: Bobphys. 288, 97-106, 1991
A;Title: Cloning and characterization of the mouse cytochrome c oxidase subunit IV gene.
A;Reseronce number: S16114; MUID:91378465; PMID:1654830
A;Accession: S16114
A;Residues: 1-169 cARC>
C;Genetics:
A;Gene ocxiv
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A.Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A.Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: G72293
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-294 <a href="https://docume.com/residues: 1-294">docume.com/residues: 1-294 <a href="https://docume.com/residues: 1-294">docume.com/residues: 1-294 <a href="https://docume.com/residues: 1-294">docume.com/residues: 1-294 <a href="https://docume.com/residues: 1-294">docume.com/residues: 1-294 <a href="https://docume.com/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/residues/r
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: G72293
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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C:Species: Thermotoga maritima
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34.3%; Score 48; DB 1; Length 169;

Best Local Similarity 36.4%; Pred. No. 7.2;

Matches 8; Conservative 5; Mismatches 9; Indels
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122 SVMEIPDFPRPLIIS 136
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Query Match
Best Local Similarity 35.3%;
Matches 6; Conservative ...
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Matches 9; Conservative
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hypothetical protein alr7383 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120al C; Species: Nostoc sp. PCC 7120

C; Species: Nostoc sp. PCC 7120

A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C; Accession: AGESES

R; Kaneko, T: Nakamura, Y: Wolk, C.P.; Kuritz, T: Sasamoto, S:; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S:; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA, Ress B, 205-213, 2001

A; Reference number: AB1807; MUID:21595285; PMID:11759840

A; Reference number: AGESES

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-222 «KUR»

A; Residues: 1-222 «KUR»

A; Residues: 1-224 «KUR»

A; Residues: 1-232 «KUR»

A; Residues: 1-232 «KUR»

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S.; Smith, Ho.J. Venterback, T.; Zalewski, C.; Ma
S.; Smith, Ho.J. Venterback, T.; Zalewski, C.; Ma
S.; Smith, Ho.J. Venterback, T.; Zalewski, C.; Ma
A.Recence number: J.S.; MulD:20036896; PMID:10567266
A.Accession: C.S.S.
A.Status: preliminary
A.Molecule Lype: DNA
A.Residues: 1-433 *WHI>
A.Residues: 1-433 *WHI>
A.Residues: 1-433 *WHI>
A.Residues: 1-434 *WHI>
A.Residues: 1-535 *WHI>
A.Residues: 1-535 *WHI>
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A.Residue
Extremophiles 2, 417-425, 1998
A;Title: Genetic profile of pNOB8 from Sulfolobus: the first conjugative plasmid from an A;Title: Genetic profile of pNOB8 from Sulfolobus: the first conjugative plasmid from an A;Reference number: 220959; MUID:99044580; PMID:9827331
A;Accession: T31043
A;Accession: T31043
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-165 <AHE>
A;Cross-references: EMBL:AJ010405; NID:e1351926; PID:e1351965; PIDN:CAA09149.1
C;Genetics:
A;Genome: plasmid pNOB8
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C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
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43.8%; Pred. No. 7.2;
tive 5; Mismatches
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Best Local Similarity 43.8
Matches 7; Conservative
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phosphoribosylformylglycinamidine synthase II (purl) PAB1201 - Pyrococcus abyssi (strain c) Species: Pyrococcus abyssi (c) Species: Pyrococcus abyssi (c) Species: Pyrococcus abyssi (c) Species: O-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000 (c) Accession: A75026 R; anonymous, Genoscope R; anonymous, Genoscope Bublitee of the EMBL Data Library, July 1999 A; Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stra A; Reference number: A75001
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A, Molecule type: DNA
A, Molecule type: DNA
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A, Molecule type: DNA
A, Molecule type: DNA
A, Residues: 1-363 < FEBL>
A, Cross-references: EMBL: X59720; NID: 91907116; PIDN: CAA42310.1; PID: 91907162; GSPDB: GNO
R, Tohe-, A.; Sahashi, Y.
R, Tohe-, A.; Sahashi, Y.
A, Title: The PET18 locus of Saccharomyces cerevisiae: a complex locus containing multip
A, Reference number: S07692; MUID: 89131254; PMID: 3916862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Accession: A75026
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-705 <KAW>
A;Residues: 1-705 <KAW>
A;Cross-references: GB:AJ248288; GB:AL096836; NID:G5458960; PIDN:CABS0647.1; PID:G54591:
A;Experimental source: strain Orsay
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NyAlternate names: protein YCR019w
C;Species: Saccharomyces cerevisiae
C;Date: 30-Jun-1991 #sequence_revision 30-Sep-1993 #text_change 16-Jun-2000
C;Accession: S19429; S07695
R;Peldmann, H; Mannhaupt, G.; Vetter, I.
R;Peldmann, B; Squence Database, March 1992
A;Reference number: S19429
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Length 433,
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Pred. No. 14;
3; Mismatches 5;
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A;Residues: 1-14,'I',15-81,83-282,'S',284-363 <TOH>
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Pred. No. 25;
2; Mismatches
  Score 49; DB 2
Pred. No. 14;
7; Mismatches
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A;Cross-references: SGD:S0000612; MIPS:YCR019w
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117 EAVAQRPDLPEPLLRQL 133
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Local Similarity 55.0%;
les 11; Conservative
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A; Molecule type: mRNA
A; Residues: 'N',169-307,'L',309-342 <KIN>
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l
C; Superfamily: immunoglobulin C region; immunoglobulin homology
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;19-80/Domain: immunoglobulin homology <IMI>
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Fi223-294/Domain: immunoglobulin homology <IM3>
Fi237-389/Domain: immunoglobulin homology <IM4>
Fi327-389/Domain: immunoglobulin homology <IM4>
Fi46,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predict
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A. Accession: A93442
A. Molecule type: mRMA
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                C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C;Accession: S38864
B;Xipp, B: Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A;Pescription: Combination of a defined specificity and desired isotype by cloning of A;Reference number: S38864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Dec-1982 #sequence revision 17-Dec-1982 #text_change 16-Jul-1999
C;Accession: A33442, A90937; A02143
R;Hellman, L.; Pettersson, U.; Engstrom, A.; Karlsson, T.; Bennich, H.
Nucleic Acids Res. 10, 6041-6049, 1982
A;Title: Structure and evolution of the heavy chain from rat immunoglobulin E.
A;Reference number: A93442; MUID:83064537; PMID:6292865
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C;Species: Sulfolobus sp.
C;Dactes 02-56p-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000
C;Accession: T31043
R;She, Q.; Phan, H.; Garrett, R.A.; Albers, S.V.; Stedman, K.M.; Zillig, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross_references: EMBL:227397; NID:9416537; PIDN:CAA81788.1; PID:9940782
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;353-421/Domain: immunoglobulin homology <IMM>
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Pred. No. 4.1e-05;
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Mismarches 2;
          epsilon chain C region - mouse (fragment)
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Best Local Similarity 77.3%;
Matches 17; Conservative (
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Best Local Similarity 90.9
Matches 20; Conservative
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A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-548 <KIP>
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Rilu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D.H.
Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982
A;Title: Cloning and nuclectide sequence of mouse immunoglobulin epsilon chain cDNA.
A;Reference number: A02144; MUID:83117774; PMID:6818553
A;Residues: A02144; MUID:83117774; PMID:6818553
A;Residues: L-388 «LIU»
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1GB Chain C3 region - mouse (fragment)

C.Species mausculus (house mouse)

C.Species musculus (house mouse)

C.Accession: 168726

R.Shinkal, Y.; Makauchii, H.; Honjo, T.; Okumura, K.

Immunogenetics 27, 288-292, 1988

A;Title: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid &

A;Reference number: 154443; MUID:88152907; PMID:3346043

A;Reference mumber: 154443; MUID:88152907; PMID:3346043

A;Accession: 168726

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-107 < RES-

A;Cross-references: GB:M22930; NID:9194455; PIDN:AAA37911.1; PID:9194460

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;22-90/Domain: immunoglobulin homology < IMM>
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Species: Mus musculus (house mouse) /
Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
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Best Local Similarity 90.9%; Pred. No. 2.5e-09;
Matches 20; Conservative 0; Mismatches 2; Indels
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F;22-90/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 90.9%
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RESULT 5 S38864

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

February 26, 2004, 08:18:56; Search time 10 Seconds (without alignments) 240.479 Million cell updates/sec Run on:

140 1 CGYGYQSIVDRPDFPKPIVRSITLC US-09-701-623C-8 Title: Perfect score: Sequence:

25

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 segs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	SUMMARIES	Description		I68730 IgE chain C3 regio	chain C3	Ig epsilon ch	psilon	EHRT Ig epsilon chain (hypothetical	conserved hyp														Ig e		11 probable	628 hypothetical prote	40 adenine	706 probable enovl-Coi	,
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		Length	423	107	107	388	548	429	165	232	433	705	363	169	294	1259	169	241	591	914	210	172	351	359	426	430	705	715	172	294	
	dK	당성	82.9	77.1	77.1	77.1	77.1	60.7	35.0	35.0	35.0	35.0	34.6	34.3	34.3	34.3	33.6	33.6	33.6	33.6	33.2	32.9	32.9	32.9	32.9	32.9	32.9	32.9	32.1	32.1	
100 100 100 100 100 100 100 100 100 100		Score		0	0	0	0	85	49	4	49	4	48.5	4.8	48	48	47	47	47	47	46.5	46	46	46	46	46	46	46	4 N	4	
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C)Accession: I68730
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
R;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
M;Shinkai, Y.; Nakauchi, H.; Honjo, T.; Okumura, K.
A;Tile: Mouse immunoglobulin allotypes: Multiple differences between the nucleic acid A;Reference number: I54443; MUID:88152907; PMID:3346043
A;Reference number: I54443; MUID:88152907; PMID:3346043
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A;Reference number: I5673

A;Cross-references: GB:M22933; NID:g194464; PIDN:AAA37915.1; PID:g194469 C;Superfamily: immunoglobulin C region; immunoglobulin homology

IgE chain C3 region - mouse (fragment) C;Species: Mus musculus (house mouse) C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 21-Jan-2000

281 GYGYQCVVDRPDFPKPIVRSITL 303

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RESULT 2

NADH dehydrogenase NADH2 dehydrogenas	transcription fact statherin precurso	beta-amylase (EC 3 phosphoesterase-re	hypothetical prote probable membrane	pol protein - simi cytochrome-c oxida	translation initia L-ascorbate oxidas	probable DNA repli elongation factor	P-type ATPase - sl
H85868 A65000	A10/96 G02326 SBHUP	S38779 A87198	T16904 S55151	D49281 OLBO4	T39767 KSKVAO	B72775 D83112	T30580
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32.1	32.1 31.8	31.8	31.8	31.4	31.4	31.4	31.4
4.4. N N	44 44. 70.70	4.4. 4.4. 0.5.	44. 44.5	4 4 4 4	44	4, 4 4, 4	44
30	2 6 6 2 6 4	35 36	37	3.9 4.0	4 4	4.4 6.4	4.5

ALIGNMENTS

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Time position chain C region (version 2) - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Species: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996 (Spacession: A02145 ) (Species: 31-3144 ) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31-3144) (Species: 31444) (Species: 31
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C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kajintrons: An immunoglobulin heterotetramer subunit consists of two identical light (kajint disulfide bonds. In some cases, such as 1gA and 1gM, the subunits associate into 1 C; Superfamily: immunoglobulin cregion; immunoglobulin homology clMM1>
C; Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin homology clMM1>
F; 125-183 Domain: immunoglobulin homology clMM2>
F; 220-288 Domain: immunoglobulin homology clMM3>
F; 225-286 Domain: immunoglobulin homology clMM3>
F; 225-181, 227-286, 332-394 /Disulfide bonds: #status predicted
F; 43, 84, 167, 239, 262, 417/ Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 GYGYQSIVDRPDFPKPIVRSITL 24
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Best Local Similarity 91.3°
EHMSS
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71.0%; Score 103; DB 3; Length 45;
Best Local Similarity 68.0%; Pred. No. 5.1e-09;
Matches 17; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                          71.0%; Score 103; DB 3; Length 45
68.0%; Pred. No. 5.1e-09;
tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
FILING DATE: 30-APR-1999
CLASSIFICATION:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-UUR-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MATIAH 1. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMONICATION INFORMATION:
TELECHONE: 212-758-4800
TELEFRAX: 212-758-4800
INFORMATION FOR SEQ ID NO: 101: SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-7UNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: MATHE H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECHONE: 212-758-4800
TELEFAX: 212-758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 101, Application US/09303323
Sequence 101, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: INMUNOENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 CGETYQSRVTHPHLPRALMRSTTKC 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTER.STICS:
TRNGTH: 45 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 68.0%
Matches 17; Conservative
                                                                                                                                                                                                                                                                                            TYPE: amino acid

' TOPOLOGY: linear

' MOLECULE TYPE: peptide

US-09-100-4148-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: amino acid
; TOPOLOGY: linear
; MOLEGULE TYPE: peptide
US-09-303-323-101
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                                                                                                                                                                                                                                                       Sequence 101, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: INWINGEN:
ITILE OF INVENTION: INWINGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: February 26, 2004, 08:29:26 Job time : 12.6 secs
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STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MURDIUM TYPE: FIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIPICATION NUMBER: 09/100,414
FILING DATE: 20-UNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECHONE: 212-758-4800
TELECHANCE/CATION INFORMATION:
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TELECHANCE/CATION INFORMATION:
TELECHANCE/CATION INFORMATION:
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21 CGETYQSRVTHPHLPRALMRSTTKC 45
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INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
1.RNGTH: 45 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 10154-0054
ZIP: 10154-0054
COMPUTER READABLE FORM:
TITTIM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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Length 42;
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Best Local Similarity 68.0%; Pred. No. 4.8e-09;
Matches 17; Conservative 3; Mismatches 5;
                    Sequence 100, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
TITLE OF INVENTION: IMMUNOGENS
INVERS OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSES: Morgan & Finnegan, L.L.P.
STRRET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 111, Application US/09100414B
Patent No. 6025468
GENERAL INFORMATION:
TITLE OF INVENTION: INMUNOGENS
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Pinnegan, L.L.P.
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCENARIA STATES OF TANAMARES SCENARIA SECTION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIPICATION NUMBER: US/09/770,014
FILING DATE: 20-UNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECHONE: 212-758-4800
TELECHONE: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 CGETYQSRVTHPHLPRALMRSTTKC 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                     Length 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 71.0%; Score 103; DB 4; Length 42 Best Local Similarity 68.0%; Pred. No. 4.8e-09; Matches 17; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                 Query Match
71.0%; Score 103; DB 4;
Best Local Similarity 68.0%; Pred. No. 4.8e-09;
Matches 17; Conservative 3; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secondary Control of Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secondary Secon
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REFERENCE/DOCKET NUMBER: 1151-4157
RELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPHONE: 212-758-4800
INFORMATION FOR SEQ ID NO: 99:
SEQUIENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGEGYOSRVDHPHFPKPIVRSITKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18 CGETYOSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                 TELEPHONE: 212-758-480.
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTER.STICS:
LENGTH: 42 amino acids
                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-98
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MOLECULE TYPE: peptide
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US-09-770-014-99
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SOFTWARE: Word 97
CURRENT APPLICATION DATA:

RESULT 12

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COMPUTER: 0.054

ZIP: 10154-0054

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1EM PC COMPATIBLE
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97

CURRENT APPLICATION NUMBER: US/09/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: WORG 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGRAT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
: 345 Park Avenue
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-100
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                                                           USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-09-770-014-98
                                                             COUNTRY:
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               Length 42;
               Ouery Match 71.0%; Score 103; DB 3; Length 42 Best Local Similarity 68.0%; Pred. No. 4.8e-09; Matches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5; Indels
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68.0%; Pred. No. 4.8e-09;
tive 3; Mismatches 5.
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TITLE OF INVENTION: INMUNOGENS

TITLE OF INVENTION: INMUNOGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 100, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:

COUNTRY:

CONTUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC Windows

SOFTWARE: Word 97

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/303,323

FILING DATE: 30-APR-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/100,414

FILING DATE: 20-UNE-1998

ATTORNEY AGENT INFORMATION:

NAME: MARIA H. LIN

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4157

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION NUMBER: 1151-4157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
                                                                                                1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                          18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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                                                                                                                                                                                                                                        Sequence 99, Application US/09303323
Patent No. 6228987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 99: SEQUENCE CHARACTERISTICS: LENGTH: 42 amino acids TYPE: amino acids TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 68.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // TOPOLOGY: linear
// MOLECULE TYPE: peptide
US-09-303-323-99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
US-09-303-323-100
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5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 98, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: INMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, I.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-UUNE-1998
ATTOKNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAK: 212-754-6490
INFORMATION FOR SEQ ID NO: 100:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6228987

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: IMMUNGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: DS/9/9/303,323
FILING DATE: 30-APR-1999
CLASSIFICATION NUMBER: US/9/303,323
FILING DATE: 30-APR-1999
ATTONEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEPHONE: 212-758-6849
INFORMATION POR SEQ ID NO: 98:
SEUTENCE OF TRANSCRESSIFICES:
CENTRAL OF THE SECOND OF TELEPHONE: 212-758-6849
INFORMATION POR SEQ ID NO: 98:
SEQUENCE CHRARACTERISTICS:
CENTRAL OF SEQ ID NO: 98:
SEQUENCE CHRARACTERISTICS:
CENTRAL OF SEQ ID NO: 98:
SEQUENCE CHRARACTERISTICS:
CENTRAL OF SEQ ID NO: 98:
1 CGEGYOSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear, MOLECULE TYPE: peptide US-09-100-414B-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                    STATE: NY
COUNTRY: USA
ZUNTRY: USA
ZUNTRY: USA
ZUNTRY: USA
ZUNTRY: USA
ZUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM FC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION DATA: 20,00,414B
FILING DATE: 20-UUNE-1998
CLIASSIPFORTION NUMBER: US/09/100,414B
FILING DATE: 20-UUNE-1998
CLIASSIPFORTION NUMBER: 121-1998
TILING DATE: 20-TWHENE: 1151-4157
REPERRNUE/DOCKET NUMBER: 1151-4157
TELEFORMUNICATION INFORMATION:
TELEFORMEN: 212-758-4800
TELEFORM: 212-751-6849
INFORMATION FOR SEQ ID NO: 99:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-100-414B-100

Sequence 100, Application US/09100414B

Patent No. 6025468

GENERAL INFORMATION:

APPLICANT: Wang, Chang Yi

TILLE OF INVENTION: NOVEL LHRH PEPTIDE;

TITLE OF INVENTION: IMMUNGENS

NUMBER OF SEQUENCES: 106

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: NY

STREET: NY

COUNTRY: USA
                                                                                                                            RESULT 5
US-09-100-414B-99
| Sequence 99, Application US/09100414B
| Patent No. 6025468
| GENERAL INCPRATION:
| TITLE OF INVENTION: IMMUNOCEN:
| TITLE OF INVENTION: IMMUNOCEN:
| NUMBER OF SEQUENCES: 106
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: MORGAN & Finnegan, L.L.P.
| STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CGEGYOSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                    18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 68.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-100-414B-99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 71.0%; Score 103; DB 4; Length 25 Best Local Similarity 68.0%; Pred. No. 2.7e-09; Matches 17; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 98, Application US/091004148
; Sequence 98, Application US/091004148
; Patent No. 6025468
; GENERAL INFORMATION:
APPLICANT: Wangy Chang Yi
TITLE OF INVENTION: NOVEL LIHRH PEPTIDE;
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDR
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APPLICATION NUMBER: US/09/770,014
                      FILING DATE:
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAWE: MARIA H. Lin
REGISTRATION NUMBER: 29,323
REFRENCE/DOCKET NUMBER: 1151-415
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBRAR: 212-758-4800
TELEBRAR: 212-751-6849
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 antho acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CGETYQSRVTHPHLPRALMRSTTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIPIE: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,4
FILING DATE: 20-UUNE-1998
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAXIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-
TELECOMMOTICATION INFORMATION:
TELECOMMOTICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 98:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 42 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: peptide US-09-770-014-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                        Squence 95, Application US/09770014
Patent No. 6559282
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                            GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: INVORE LHRH PEPTIDE
TITLE OF INVENTION: INVUNOGENS
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CGEGYQSRVDHPHFPKPIVRSITKC 25
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COUNTRY: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compartible
COMPUTER: BY PC compartible
COMPUTER: WOR'S 97
CURRENT APPLICATION DATA:
                   Sequence 95, Application US/09303323
Patent No. 6228987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-303-323-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
US-09-770-014-95
   US-09-303-323-95
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Sequence Sequence Sequence

Sequence 19, Appli Sequence 1, Appli Sequence 11, Appli Sequence 19, Appl Sequence 20, Appl Sequence 18, Appl Sequence 17334, A Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 11, Appli

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Query Match 71.0%; Score 103; DB 3; Length 25; Best Local Similarity 68.0%; Pred. No. 2.7e-09; Matches 17; Conservative 3; Mismatches 5; Indels
US-08-232-539D-54
US-08-232-539D-56
US-09-479-614-14
US-09-479-614-29
US-09-479-614-29
US-08-464-025A-1
US-08-466-163B-1
US-08-802-096-1
US-08-802-096-1
US-08-232-539D-19
US-08-232-539D-18
US-08-232-539D-18
US-08-232-539D-18
US-08-466-151-1
                                                                                                                                                                                                                                                US-08-289-942A-7
US-08-890-719-12
US-08-890-719-11
                                                                                                                                                                                                                                                                                                                                                                                              US-09-100-414B-95; Sequence 95, Application US/09100414B; Patent No. 6025468; PAPPLICANT: Wang, Chang Yi; TITLE OF INVENTION: NOVEL LHRH PEPTIDE; TITLE OF INVENTION: IMMUNOSENS; NUMBER OF SEQUENCES: 106 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: NEW TOLK
STATE: NEW TOLK
STATE: NEW TOLK
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURKENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,414B
FILING DATE: 20-JUNE-1998
CLASSIFICATION: 424
ATTORNEY AGENT INFORMATION:
NAME: MATIA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELECOMMUNICATION INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
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     US-09-100-414B-95
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99, Appl
99, Appl
100, App
98, Appl
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100, App
101, App
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101, App
96, Appl
97, Appl
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96, Appl
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97, Appl
97, Appl
                                                                                                                 Pebruary 26, 2004, 08:19:31 ; Search time 12.6 Seconds
(without alignments)
102.432 Million cell updates/sec
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. /cgnZ 6/ptodata2/jaa/5A_COMB.pep:*
. /cgnZ 6/ptodata2/jaa/5B_COMB.pep:*
. /cgnZ 6/ptodata2/jaa/6A_COMB.pep:*
. /cgnZ 6/ptodata2/jaa/6B_COMB.pep:*
. /cgnZ 6/ptodata2/jaa/BCCOMB.pep:*
. /cgnZ 6/ptodata2/jaa/PCTUS_COMB.pep:*
. /cgnZ 6/ptodata/2/jaa/PCTUS_COMB.pep:*
                    GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-370-223-95
US-09-370-223-95
US-09-100-414B-98
US-09-100-414B-99
US-09-303-323-99
US-09-303-323-99
US-09-303-323-99
US-09-370-014-98
US-09-770-014-99
US-09-770-014-99
US-09-770-014-99
US-09-770-014-99
US-09-770-014-99
US-09-100-414B-101
US-09-100-414B-97
US-09-303-323-96
US-09-373-323-97
US-09-373-323-97
US-09-373-323-97
US-09-373-323-97
US-09-370-014-98
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1 CGEGYQSRVDHPHFPKPIVRSITKC 25
                                                                                                                                                                                                                                                                                                   389414 seqs, 51625971 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                     - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match
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Perfect score:
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Maximum DB
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AAY91228-Y91231 represent CETP-derived peptides and AAY91232-Y91241 are immunogens comprising a CETP peptide and a Th epitope which may be used to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising MVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. (Updated on 12-SEP-2003 to standardise OS field)
          88888888888888
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Sequence 46 AA;

Gaps o O Query Match
Best Local Similarity 100.0%; Pred. No. 2.9e-14;
Matches 25; Conservative 0; Mismatches 0; Indels

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Search completed: February 26, 2004, 08:23:33 Job time : 48.6 secs

Promiscuous T-cell epitope, measles virus F protein, MVF, hepatitis B virus surface antigen, HBV, immunogenic; B-cell epitope; luteinising hormone releasing hormone, LHRH, contraceptive, anticancer, somatostatin, growth promotion; CD4 receptor, HIV-1; antiviral, FMDV, foot and mouth disease virus, immunoglobulin E; IgE; anti-allergic, Plasmodium falciparum; circumsporozoite; antimalarial, CETP;

Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:93

cholesteryl ester transport protein; anti-arteriosclerotic

Measles virus

sapiens

Chimeric.

W09966957-A2 29-DEC-1999

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The specification describes peptide immunogens comprising a synthetic releasing hormone teleasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, cestrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostent or breast, also endometriosis); to prevent boar taint (and appears in the specification
breast cancer; endometriosis; boar taint; meat quality; immunocastration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New peptide immunogen containing luteinizing hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Scor.
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 93; 102pp; English
                                                     Location/Qualifiers
                                                                                                                                                                                                   label= Lys, Arg
                                                                                 'label= Ser, Thr
                                                                                                             label= Lys, Arg
                                                                                                                                                                                                                               /label= Gly, Thr
                                                                                                                                                                                                                                                                                                                                                                           (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                 98US-00100414.
                                                                                                                                                                                                                                                                                                                     99WO-US013960.
                                                                                                                                         label= Gly,
                                                                                                                                                                      label= His,
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-160562/14.
                                                                                                                                                          Misc-difference
                                                                                                                                                                                    Misc-difference
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                                                                                                                            Misc-difference
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                        Unidentified
                                                                                                                                                                                                                                                           WO9966952-A1
                                                                                                                                                                                                                                                                                                                     21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                 20-JUN-1998;
                                                                                                                                                                                                                                                                                        29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                          Wang CY;
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New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.

(UNBI-) UNITED BIOMEDICAL INC

20-JUN-1998;

WPI; 2000-160564/14.

Wang CY;

99WO-US013975 98US-00100412.

21-JUN-1999;

Example 6; Page 98; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the The epitopes of the invention of and immunogenic peptides comprising the The epitopes and peptide immunogens containing them, are used to induce a T helper cell response.

Containing them, are used to induce a T helper cell response, epetidically against Plasmodium falciparum, cholesteryl ester transport protein (ESTP) or HIV epitopes, but more generally against any pethosen; immunogens may be used for prevention and/or treatment of peptide immunogens may be used for prevention and/or treatment of homone inferions (HIV) foot-and-mouth disease or malaxia); for cancer immunotherapy; for inhibition of the action of luteinising hormone (InHM) for contraception, treatment of hormone releasing hormone (InHM) for contraception, treatment of hormone releasing hormone (InHM) for contraception, treatment of hormone arteriographic and peptides subjects) into an immunogen improves capacity to arteriosclerosis. Incorporation of a promiscuous improves capacity to content of antihodise subjects) into an immunogen improves capacity to conduction of antihodise against a target antiqen. The can replace criterior production of antihodise against a target antiqen. The can appropriated Thelper epitope from the measles virus F (MVF) protein and sequences AMY91124. PAY9125 and AMY91245. Pay1246 protein and sequences AMY91144. Pay10ps from the measles virus (HWF) protein and sequences AMY91144. Pay10ps from the measles virus (HWF) surface antigenic peptides comprising an inHMB sequence joined to a promiscuous Th epitope from the MYP antigenic peptides comprising an inHMB sequence joined to a promiscuous Th epitope (AMY91135 are partigenic peptides of promiscuous Th epitope/AMY91137 is the LHMH target antigenic peptides of prevent HWF) infection of a human rige (immunogens may be used to prevent HWF) may a human rige (immunogens and AMY91221. Pay1041. PAY91201 are MYH Th epitope/CACC resement of a human rige (immunogens and p

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Length 46;

Score 140; DB 3; Length 4 Pred. No. 2.9e-14; Mismatches 0; Indels

1 CGETYQSRVTHPHLPRALMRSTTKC 25

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Query Match Best Local Similarity 100.0 Matches 25; Conservative

CGETYQSRVTHPHLPRALMRSTTKC

22

RESULT 15 AAY91213

AAY91213 standard; peptide; 46 AA.

(revised)
(first entry)

12-SEP-2003 22-MAY-2000

AAY91213;

axaxata Xaakxa

46

us-09-701-623c-5.rag

Unidentified WO9967293-A1 29-DEC-1999,

Wang CY,

15-MAY-2000

AAY80007;

RESULT 12

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The present sequence is that of a synthetic immunogenic peptide derived from human IgS. This is an example of peptides that can be used in claimed immunostrimulatory complexes of the invention that are specifically adapted to act as adjuvant and as peptide immunogen stabiliser. The complexes comprise a CpG oligonucleotide and a biologically active peptide immunogen. The complex is particulate and can efficiently present peptide immunogen. The complex is particulate and can oproduce an immune response. The complexes may be prepared with various ratios of peptides to CpG oligonucleotides to provide different physical properties, such as the size of the microparticle. An immunostimulatory complex comprising the present IgE derived peptide can be used in an anti-IgB immunotherapeutic vaccine for the treatment of allergy.
                                                                                                            Immunostimulant; vaccine; human; immunogen; IgE; immunotherapy; allergy;
antibody; antiallergic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Helper T cell epitope, peptide immunogen; LHRH;
luteinising hormone-releasing hormone; spermatogenesis; ovulation;
osetrus; sexual development; sex hormone; promiscuous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stabilized immunostimulating complex, useful for vaccination, e.g. against human immune deficiency viruses, comprises cationic peptide immunogen and anionic oligonucleotide.
                                                         IgE peptide used in immunostimulant complex for allergy vaccine.
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100.0%; Score 140; DB 7;
Best Local Similarity 100.0%; Pred. No. 2.8e-14;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 20; SEQ ID NO 11; 159pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-FEB-2003; 2003WO-US004711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-FEB-2002; 2002US-00076674
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29-JAN-2004 (first entry)
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                                                                                                                                                                                                                                                                                                  Key
Modified-site
                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                         Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigenic peptides (1). (1) have anti-allergic, anti-anaphylattic and antigenic peptides (1). (1) have anti-allergic, anti-anaphylattic and antigenic peptides (1) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of 1gB, and so a target effector site on the epsilon-heavy chain of 1gB, and so containing triggering and activation of mast cells and basophils and downregulation of 1gB synthesis. Conjugates, or fusion peptides, containing (1) are used for active immunisation against 1gB-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermartitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope conjugates of (1) that include a promiscuous T helper cell epitope conjugates of (1) that include a promiscuous T helper cell epitope conjugates of (1) that include a promiscuous T helper cell epitope conjugates of (1) that include a promiscuous T helper cell epitope conjugates of (1) that include a promiscuous T helper cell epitope conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of (1) that include a promiscuous T helper cell epitope. Conjugates of
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0
                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; immunoglobulin immunostimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergy disease; immunisation; anti-allergic; anti-asthmatic; asthma; anaphylactic; atti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antigenic peptide from the CH3 domain of immunoglobulin E, fusions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention describes immunoglobulin E (IgE) - CH3 domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,10
                                                                                                                                                                                                                                                                                               IgE-CH3 domain antigen peptide antigenic site 15b SEQ ID NO:14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 140; DB 3; Length 45; 100.0%; Pred. No. 2.8e-14; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; Page 75; 155pp; English.
                                                                                                                   AAY80007 standard; peptide; 45 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for immunization against allergy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UNBI-) UNITED BIOMEDICAL INC
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                                                                                                                                                                                                                                   (first entry)
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nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walfield AM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUN-1999;
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Query Match Best Local Si Matches 25,

ADD89951

RESULT 13

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Length 45; Indels (UNBI-) UNITED BIOMEDICAL INC

98US-00100412

20-JUN-1998;

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                                                                                                                                                                                                         The specification describes peptide immunogens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormonereleasing hormone (LHR). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of spermatogenesis, ovulation, cestrus, sexual development and secretion of sex hormones. Provision of a promiscous T helper epitope (which is functional in genetically diverse subjects) provides optimum munogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as invention are used to vaccinate against mammalian LHRH, for use as provation to the present tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and immunocent meat quality) and for immunocastration. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Promiscuous T-cell epitope, measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive, anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IgE; anti-allergic; Plasmodium falciparum; circumsporozoite; antimalarial; CBTP;
                                                                                                                                      New peptide immunogen containing luteinizing hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 140; DB 3; Length 45; 100.0%; Pred. No. 2.8e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cholesteryl ester transport protein; anti-arteriosclerotic
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modified HBV surface Ag/IgE CH3 domain, SEQ ID NO:98.
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 CGETYÓSRVTHPHLPRALMRSTTKC 45
                                                                                                                                                                                      Disclosure; Page 95; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY91218 standard; peptide; 45 AA.
                                                                   (UNBI-) UNITED BIOMEDICAL INC
                       99WO-US013960.
                                              98US-00100414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US013975.
                                                                                                                                                                                                                                                                                                                                                               appears in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
Local Similarity 100...
                                                                                                                WPI; 2000-160562/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hepatitis B virus.
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens.
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                       21-JUN-1999;
                                              20-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-SEP-2003
22-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY91218;
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                                                                                         Wang CY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the The pitopes of the irvention and immunogenic peptides comprising the The pitopes of the irvention calong with B cell epitopes. The Th epitopes and peptide immunogens containing them are used to induce a T helper cell response.

CC containing them are used to induce a T helper cell response.

Specifically against Plasmodium falciparum, cholesteryl ester transport protein (CETP) or HIV epitopes, but more generally against any pathogen, immunoseative self-antigen or tumour and/or treatment of cancer infections (HIV, foot-and-mouth disease or malaria) for cancer infections (HIV, foot-and-mouth disease or malaria) for cancer infections (HIV, foot-and-mouth disease or malaria) for cancer infections (HIV, foot-and-mouth disease or malaria) for cancer infections (HIV, foot-and-mouth disease or malaria) for cancer infections (HIV, foot-and-mouth disease or malaria) for cancer releasing hormone (LHRB) for contraception, treatment of hormone-releasing the growth of animals; or for treatment of hormone-control of a promiseous infections (HIV) foot-and-mouth disease or immunoseation of a promiseous of a promiseous infection of a promiseous infection of a promiseous of a promiseous infection of animals; or for treatment of hormone-control of animals; or for treatment of hormone-control of animals; or foot-and-mouth helper epitope from the measles virus propersent syntheric The piper epitope from the measles virus (HVP) surface anticenic peptides comprising an IMRH sequence AMY91122-19142, AMY91120 sometocratin and equences AMY91137 is the IMRH target antigenic peptides comprising sometocratin and equence of animals of measure antigenic peptides comprising sometocratin malar entidence of peptides. AMY91201-191107 and AMY91201-191107 are antigenic peptides comprising sometocratic and mouth epitope/LGE cancer antigenic peptides on the MIVE of CCC AMY91201-191107 are mutigenic peptides comprising sometocratic or an und
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to prevent or treat arteriosclerosis and cardiovascular disease. AAY91247 and AAY91252-Y91257 are HIV-1 neutralising B-cell epitopes, and AAY91248-Y91251 and AAY91258-Y91273 are antigenic peptides comprising WVH Th and HIV-1 B-cell epitope which may be used as a component in an anti-HIV-1 vaccine. AAY91198 and AAY91199 are respectively an immunostimulatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invasin protein epitope from Yersinia species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                      New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                              Example 6; Page 100; 129pp; English
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                                                                                                                                                                                                      antigenic site, for immunization a or human immune deficiency virus.
                                                                      WPI; 2000-160564/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The present sequence is that of a synthetic immunogenic peptide derived from human IgE. This is an example of peptides that can be used in claimed immunostimulatory complexes of the invention that are specifically adapted to act as adjuvant and as peptide immunogen stabiliser. The complexes comprise a CpG oligonucleotide and a biologically active peptide immunogen. The complex is particulate and can efficiently present peptide immunogens to the cells of the immune system to produce an immune response. The complexes may be prepared with various ratios of peptides to CpG oligonucleotides to provide different physical properties, such as the size of the microparticle. An immunostimulatory complex comprising the present IgE derived peptide can be used in an anti-IgE immunotherapeutic vaccine for the treatment of allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                breast cancer; endometriosis; boar taint; meat quality; immunocastration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helper T cell epitope, peptide immunogen; LHPH; Ultahising hormone-releasing hormone, releasing hormone, spermacogenesis, ovulation; oestrus; sexual development; sex hormone; promiscuous T helper epitope; vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stabilized immunostimulating complex, useful for vaccination, e.g. against human immune deficiency viruses, comprises cationic peptide immunogen and anionic oligonucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 140; DB 7;
100.0%; Pred. No. 2.8e-14;
iive 0; Mismatches 0;
                                                                                                                                  /note= "Epsilon-lysine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID NO 10; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20 CGETYQSRVTHPHLPRALMRSTTKC 44
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide sequence of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY68605 standard; peptide; 45
                                                                                                                                                                                                                                                                                                                                                                                                  (UNBI-) UNITED BIOMEDICAL INC.
                                                                                                                                                                                                                                                                                                                             14-FEB-2002; 2002US-00076674.
                                                                                                                                                                                                                                                                               14-FEB-2003; 2003WO-US004711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-778890/73.
                                                                                                                                                                                   WO2003068169-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44 AA;
                                                                                      Key
Modified-site
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                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                                                                                                                                   21-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sokoll KK;
                    Synthetic
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à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes immunoglobulin E (IgE)-CH3 domain antiganic peptides (I). (I) have anti-allergic, anti-anaphylactic and antiganic peptides (I). (I) have anti-allergic, anti-anaphylactic and attigate attackmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downrequiation of IgE synthesis. Conjugates, or fusion peptides, and alergies, e.g. food allergies, asthma, anaphylaxis or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maphylactogenic) antibodies. AXY9994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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antibody; antiallergic.
                                                                                                                               Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen; hamunoglope; limmunogenic; hamunoglimulatory; carrier protein; helper T cell epitope; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; asthmatic; asthma; anaphylaxis; dermatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigenic peptide from the CH3 domain of immunoglobulin E, fusions immunization against allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IGE peptide used in immunostimulant complex for allergy vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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100.0%; Pred. No. 2.6e-14;
iive 0; Mismatches 0; Indels
                                                                                      IgE immunogenic peptide conjugate SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGETYQSRVTHPHLPRALMRSTTKC 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 76; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD89950 standard; protein; 44 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UNBI-) UNITED BIOMEDICAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US013959
                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-00100287
                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 25, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walfield AM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-160578/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 42 AA;
                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                        WO9967293-A1
                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-1999;
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                                        15-MAY-2000
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ADD89950;

ADD899

Wang CY,

New

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Gaps

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Length 44; 0; Indels

from this HBV epitope. AAY91156-Y91196, AAY91227 and AAY91242-100.0%; Score 140; DB 3; Length 42; 100.0%; Pred. No. 2.6e-14; ive 0; Mismatches 0; Indels Sequence 42 AA;

Query Match Best Local Similarity 100.03 Matches 25; Conservative

1 CGETYQSRVTHPHLPRALMRSTTKC 25 18 CGETYQSRVTHPHLPRALMRSTTKC 42 ò d

AAY91217 standard; peptide; 42 AA. AAY91217; RESULT 7 AAY91217

Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:97. (revised)
(first entry) 12-SEP-2003 22-MAY-2000

Promiscuous T-cell epitope, measles virus F protein, MVF; hepatitis B virus sufface antigon; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin B; IgB; anti-allergic; Plasmodium falciparum; circumsporcoxie; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.

Measles virus. sapiens. Chimeric Ношо

WO9966957-A2.

29-DEC-1999,

21-JUN-1999;

98US-00100412. 20-JUN-1998;

(UNBI-) UNITED BIOMEDICAL INC

Wang CY;

New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.

WPI; 2000-160564/14.

Example 6; Page 99; 129pp; English.

The invention relates to novel promiscuous T helper cell epitopes (Th), and minogenic peptides comprising the Th epitopes of the invention along with B cell epitopes. The The pitopes and peptide immunogenic containing them, are used to induce a T helper cell response, containing them, are used to induce a T helper cell response, containing them, are used to induce a T helper cell response, containing them, are used to induce a T helper cell response and correct immunotenestrive self-antibition of the action of lute single hormone induced immunosens may be used for prevention and/or treatment of infections (HIV, foot-an-onuth disease or malaria); for cancer immunotenerapy; for cancer immunotenerapy; for inhibition of the action of lute initial hormone induced in the contraception, treatment of hormone induced in the contraception, treatment of hormone induced in the contraception, treatment of hormone induced in the contraception of particular of a promiscuous Th (Eurotomatic) in a recipient of a minimulation of antibodies and induced capacity in the propertion of a promiscuous Th (Eurotomation of antibodies apalmed a target antigment or production of antibodies apalmed a target antigment or production of antibodies apalmed a target antigment or particular and sequences AV91142-99126 and AA99124 sequence AA99132 and adaptione based on the WRF Th epitope sequence AA99132 and AA99124 are antigment opeptides to produce the measure of longer of captived from these LHRH antigenic peptides comprising an LHRH sequence of longer of a promiscuous Th epitope. AV99116 and AA99120 and AA9 hinge spacer peptide, nic peptides of the both of which may optionally be used in the antigenic pepti Invention. (Updated on 12-SEP-2003 to standardise OS field) protein epitope from Yersinia species, and invasin

0; Gaps

Sequence 42 AA;

Length 42; Indels 100.0%; Score 140; DB 3; 100.0%; Pred. No. 2.6e-14; ive 0; Mismatches 0; Local Similarity 100.0 Les 25; Conservative Query Match Matches

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Gaps · 0

> 25 1 CGETYQSRVTHPHLPRALMRSTTKC CGETYOSKVTHPHLPRALMRSTTKC 18

> > g ઠે

AAY80014 ID AAY8 XX RESULT 8

AAY80014 standard; peptide; 42 AA.

29-DEC-1999

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The invention relates to novel promiscuous T helper cell epitopes (Th), along with B cell epitopes. The The epitopes and peptide immunogenic containing them, are used to induce a T helper cell response, containing them, are used to induce a T helper cell response, containing them, are used to induce a T helper cell response, containing them, are used to induce a T helper cell response, containing them, are used to induce a T helper cell response, containing them are used to induce and/or treatment of immunogens may be used for prevention and/or treatment of induced immunogens may be used for prevention and/or treatment of induced immunogens may be used for prevention of the action of luteinistial hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception, treatment of hormone (LHMM) for contraception in manual or contract the contract of a produced subject) into an immunogen capacity to induce a strong the performed immunogen capacity to induce a strong the performed immunogen or produced an explaining an experience AAV91120 for sequence AAV91120 and AAV91212 and AAV91212 or production of antibodice sequences AAV91120 is omatocatatin and a produced antigenic peptides comprising an inthe sequence of AAV91120 is the LHMH target antigenic peptides of any produce of an used to pervent HIV infection peptides comprising schedules and AAV9122 comprise the C section of a human IDS (immunogenes and AAV9122 vigation and a human IDS (immunogenes and AAV9122 vigation of allegies of antigenic peptides of an expective of antigenic peptides of an expective of antigenic peptides of antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invasin protein epitope from Yersinia Species, and hinge spacer peptide, both of which may optionally be used in the antigenic peptides of the invention. (Updated on 12-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                       New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.
                                                                                                                                                                                                                                                                                                                                      Example 6; Page 99; 129pp; English.
                                                                                                                                    (UNBI-) UNITED BIOMEDICAL INC
                                                                                             98US-00100412.
                                                         99WO-US013975
                                                                                                                                                                                                                     WPI; 2000-160564/14.
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                                                       21-JUN-1999;
                                                                                             20-JUN-1998;
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Score 140; DB 3; Length 42; Pred. No. 2.6e-14;
100.0%;
Query Match
Best Local Similarity
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The invention relates to novel promiscuous T helper cell epitopes (Th),
and immunogenic peptides comprising the Th epitopes of the invention
containing them, are used to induce a T helper cell response,
containing them, are used to induce a T helper cell response,
containing them, are used to induce a T helper cell response,
containing them, are used to induce a T helper cell response,
containing them, are used to induce a T helper cell response,
containing them are used to induce a T helper cell response,
containing them as a be used for prevention and/or treatment of
immunoteactive self-antiqen or tumour antigen. The Th epitopes and
containing hormone (LHRH) for contraception of luteinising hormone
containing hormone (LHRH) for contraception, treatment of hormone
containing the growth of animals, or for treating allargies or
contracelerosis. Incorporation of a promiscuous Th (functional in
contraction of animals, or for treating allargies or
contained a strong T helper cell-mediated immune response, resulting in
contraction of antibodies against a target antigen. Th can replace carrier
control and pathogen-derived T helper epitope from the measles virus F (MVF)
control and sequences AAV91122-V91144, AXV91225 and AAV91141
crepresent synthetic Th epitopes based on the MVF Th epitopes
contrigen, and sequences AAV91144-V91155 are synthetic epitopes
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.
                                                                                                                                                                                                                                                                                                                                       Promiscuous T-cell epitope, measles virus F protein, MVF; hepatitis B virus surface antigor, HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobulin E; IGE; anti-allergic; Plasmodium falciparum; circumsporzootic, antimalarial; CETP; cholestery! ester transport protein; anti-arterioscierotic.
  Gaps
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  Indels
                                                                                                                                                                                                                                                                                                     Modified MVF Th epitope/IgE CH3 domain, SEQ ID NO:95.
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0
  0; Mismatches
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                                      1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                        42
                                                                          18 CGETYQSRVTHPHLPRALMRSTTKC
                                                                                                                                                                       Ā
                                                                                                                                                                     AAY91215 standard; peptide; 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNBI-) UNITED BIOMEDICAL INC
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                                                                                                                                                                                                                                              (revised)
(first entry)
  25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Measles virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9966957-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-1999;
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                                                                                                                                                                                                                                              12-SEP-2003
22-MAY-2000
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                                                                                                                                                                                                            AAY91215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang CY;
  Matches
                                                                                                                       RESULT 6
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Best Loca
Matches
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                                                                                                              antigenic peptides (1). (1) have amit-allergic, anti-anaphylactic and antigenic peptides (1) (1) have amit-allergic, anti-anaphylactic and antigenic peptides (1) induces polyclonal antibodies specific for a target effector site on the opsilon-heavy chain of 195, and so preventing triggering and activation of mast cells and basophils and downrequiation of 195 synthesis. Conjugates, or fusion peptides, containing (1) are used for active immunisation against 195-nediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (1) that include a promiscuous T helper cell epitope (1) target epitope, have increased immunogenicity and may include cyclic target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maphylactogenic) antibodies. AAY9994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Helper T cell epitope; peptide immunogen; LHRH;
luteinising hormone-releasing hormone; spermatogenesis; ovulation;
oestrus; sexual development; sex hormone; promiscuous T helper epitope;
vaccine; contraceptive; hormone-dependent tumour; prostate cancer;
breast cancer; endometriosis; boar taint; meat quality; immunocastration.
                                               from the CH3 domain of immunoglobulin E, fusions
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                     present invention describes immunoglobulin E (IgE)-CH3 domain
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0
                                                                                                                                                                                                                                                                                                                                         Length 25;
                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                        100.0%; Score 140; DB 3;
100.0%; Pred. No. 1.4e-14;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Ile, Met, Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                      1 CGETYQSRVTHPHLPRALMRSTTKC
                                                                                                                                                                                                                                                                                                                                                                                      1 CGETYQSRVTHPHLPRALMRSTTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide seguence of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Ile, Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY68604 standard; peptide; 42 AA
                                                          against allergy.
                                                                               Claim 1; Page 21; 155pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= His, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= Lys, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Gly, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Gly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 25, Conservative
Walfield AM;
                                             antigenic peptide
immunization again
                       WPI; 2000-160578/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference 12
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                                                                                                                                                                                                                                                                                                                  Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
Wang CY,
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The specification describes peptide immunogens comprising a synthetic releasing hormore.

releasing hormore (LHKH). The peptide immunogens cause induction of a specific immune response to LHKH which is involved in regulation of a specific immune response to LHKH which is involved in regulation of speriatogenesis, ovulation, cestrus, sexual development and secretion of speriatogenesis, ovulation, destrus, sexual development and secretion of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHKH, for use as (reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast, also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus sufface antigon; HBV; immunogenic; B-cell epitope; luteinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foct and mouth disease virus; immunoglobulin B: IgE; anti-allergic; Plasmodium falciparum; circumsporozocite; antimalarial; CETP; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New peptide immunogen containing luteinizing hormone-releasing hormone antigen site and helper \mathbb T cell epitope, for e.g. contraception and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 140; DB 3;
100.0%; Pred. No. 2.6e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18 CGETYQSRVTHPHLPRALMRSTTKC 42
                                  /label= Ile, Met, Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure, Page 95, 102pp, English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ź
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                                                                                                                                                                                                                                                                                                                           98US-00100414.
                                                                                                                                                                                                                                                      99WO-US013960
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(first entry)
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nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-160562/14
Misc-difference 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 42 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   (UNBI-) UNITED
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                                                                                                                                                                                                                                                      21-JUN-1999;
                                                                                                                                                                                                                                                                                                                               20-JUN-1998;
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22-MAY-2000
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel promiscuous T helper cell epitopes (Th), and immunogenic peptides comprising the Th epitopes of the invention calong with B cell epitopes. The Th epitopes and peptide immunogens containing them, reused to induce a T helper cell response, calong with B cell epitopes. The Th epitopes and peptide immunogens may be used to induce a T helper cell response, captured in the pitopes but mover the Th epitopes and protein (CTPP) or HIV epitopes, but mover The Th epitopes and immunogens may be used for prevention and/or treatment of infections (HIV, foot-and-mouth disease or malaria); for cancer immunotherapy; for inhibition of the action of luteinising hormone releasing hormone (LHRH) for contraception, treatment of hormone. Compared in the provention of boar taint in meat, and immunocastration); for promoting the growth of animals; or for treating allergies or for promoting the growth of animals; or for treating allergies or articularisational in genetically diverse subjects) into an immunogen improves capacity to induce a strong T helper cell-mediated immune response, resulting in
                                                                                                                        ö
(reversible) contraceptive; control of hormone-dependent tumours (cancer of prostate or breast; also endometriosis); to prevent boar taint (and improve meat quality) and for immunocastration. The present sequence appears in the specification
                                                                                                                                                                                                                                                                                                                                                   Promiscuous T-cell epitope; measles virus F protein; MVF; hepatitis B virus surface antigen; HBV; immunogenic; B-cell epitope; lucinising hormone releasing hormone; LHRH; contraceptive; anticancer; somatostatin; growth promotion; CD4 receptor; HIV-1; antiviral; FMDV; foot and mouth disease virus; immunoglobluln E; IgE; anti-allergic; cholesteryl ester transport protein; anti-arteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New artificial T helper cell epitope and derived immunogens with target antigenic site, for immunization against e.g. malaria, arteriosclerosis or human immune deficiency virus.
                                                                                                                       Gaps
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0
                                                                                           Length 25;
                                                                                                                     Indels
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                                                                                           Query Match
100.0%; Score 140; DB 3;
Best Local Similarity 100.0%; Pred. No. 1.4e-14;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                          Modified human IgE CH3 domain, SEQ ID NO:92.
                                                                                                                                                                           25
                                                                                                                                               1 CGETYQSRVTHPHLPRALMRSTTKC 25
                                                                                                                                                                  CGETYQSRVTHPHLPRALMRSTTKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 6; Page 40; 129pp; English.
                                                                                                                                                                                                                                             AAY91212 standard; peptide; 25 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-00100412.
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                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-160564/14.
                                                                Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                 RESULT 2
AAY91212
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carrier
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
production of antibodies against a target antigen. Th can replace
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                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 140; DB 3; Length 25; 100.0%; Pred. No. 1.4e-14; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Optimised IgE-CH3 domain antigen peptide for human IgE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CGETYQSRVTHPHLPRALMRSTTKC 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNBI-) UNITED BIOMEDICAL INC
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Best Local Similarity 100...
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens
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                                                                                                                                                                                                                                                                                                                                                                                    invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
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February 26, 2004, 08:16:50; Search time 46.6 Seconds (without alignments) 151.581 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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1 CGETYQSRVTHPHLPRALMRSTTKC
                                                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Minimum Match 0% Maximum Match 100% Listing first 45 summaries Geneseq 29Jan04:*

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

Post-processing:

geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

IGE immun IGE immun IGE immun IGE immun IGE immun Peptide s Modified Optimised IgE pepti Peptide s Modified Modified Peptide s Modified GE immun gE-CH3 d pepti Peptide s Modified Description AAX80014
AAG88950
AAG88950
AAY800007
AAY800011
AAY80011
AAY80011
AAY80010
AAY80010
AAY80010
AAY80010
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AAY80010
AAY80010 Aay91212 | Aay79998 (Aay68604 Aay91216 | Aay91215 | Aay91217 | Aay68602 AAY91216 AAY91215 AAY91217 AAY80014 ADD89950 AAY91218 AAY68603 AAY91214 AAY80010 **AA**Y68602 **AAY80016** AAY80013 4AY79998 AAY68604 **AAY8**0011 Length DB Query Match 100.0 140 Result Š

The specification describes peptide immunogens comprising a synthetic helper T cell (Th) epitope and a target antigen, luteinising hormone-teleasing hormone (LHRH). The peptide immunogens cause induction of a specific immune response to LHRH which is involved in regulation of specific immune response to LHRH which is involved in regulation of sex hormones. Provision of a promiscuous T helper epitope (which is functional in genetically diverse subjects) provides optimum immunogenicity to the B cell epitopes of the target antigen and thus high antibody titres against the target antigen. The peptide immunogens of the invention are used to vaccinate against mammalian LHRH, for use as

Peptide s

AAY80008 AAY80012

4AY68606

6 2 AAY460078 6 2 AAX42620 0 2 AAR33321 0 2 AAR33321 0 2 AAR3322 0 2 AAR33691 0 2 AAR32025 0 2 AAR33691 0 2 AAR35678	60 3 AAY80078 106 2 AAY32620 110 2 AAR33328 110 2 AAR33321 110 2 AAR33322 110 2 AAR33681 110 2 AAR33682 110 2 AAR33680 110 2 AAR33690 110 2 AAR33330 110 2 AAR33330 110 2 AAR33319 110 2 AAR33319 110 2 AAR33319 110 2 AAR33719 110 2 AAR35744 110 2 AAR35744	3 IgE in	0		•	Aar33321 Variant I	Aar33322 Variant I	Aar33681 Variant I	Aar33682 Variant I	Aar32025 Variant I	Aar32026 Variant I	Aar33330 Variant I	Aar33680 Variant I	Aar33691 Variant I	Aar32033 Variant I	Aar33319 Variant I	Aar33678 Variant I	Aar35744 Variant I	Aar35747 Variant I	Aar35748 Variant I	Aar35751 Variant I
		AAY80078	AAY42620	AAR32034	AAR33328	AAR33321	AAR33322	AAR33681	AAR33682	AAR32025	AAR32026	AAR33330	AAR33680	AAR33691	AAR32033	AAR33319	60		7	AAR35748	AAR35751
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		133	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117	117
	133 1111111111111111111111111111111111	56	27		29		31		33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Helper T cell epitope; peptide immunogen; LHRH; luteinising hormone-releasing hormone; spermatogenesis; ovulation; luteinising hormone; sex hormone; promiscuous T helper epitope; oscirus; sexual development; sex hormone; promiscuous T helper epitope; vaccine; contraceptive; hormone-dependent tumour; prostate cancer; breast cancer; endometriosis; boar taint; meat quality; immunocastration. New peptide immunogen containing luteinizing hormone-releasing hormone antigen site and helper T cell epitope, for e.g. contraception and treatment of cancer. Disclosure; Page 92; 102pp; English. Peptide sequence of the invention. AAY68602 standard; peptide; 25 AA. 98US-00100414. (UNBI-) UNITED BIOMEDICAL INC 99WO-US013960. (first entry) WPI; 2000-160562/14. WO9966952-Al. Unidentified 21-JUN-1999; 20-JUN-1998; 05-MAY-2000 29-DEC-1999 AAY68602; Wang CY; AAY68602

preventing IgE from binding to high affinity receptors on mast cells and basophils. The products of the invention are useful in the manufacture of a medicament for treating or prevention greeneful in the manufacture of including asthma, allergic rulnitis, gastrointestinal allergic disorders including asthma, allergic rulnitis, gastrointestinal allergies used as allergies consinophilia, conjunctivitis, glomerular nephritis, flea allergies or atopic dermatitis, in an animal, e.g. human or dog. The polynucleotide products are useful for treating IgE-mediated allergic disorders, by gene therapy. Antiqenic peptides comprising conserved amino acid residues of the CH3 domain of an IgE molecule from a second unrelated species are capable of inducing a high titre of anti-IgE antibodies when administered to an animal without causing anaphylaxis. ABG74772-ABG74785 represents polypeptide sequences used in designing the constructs described in the disclosure of the invention 8888888888888888888

Sequence 346 AA;

Gaps ô 83.7%; Score 118; DB 6; Length 346; 95.7%; Pred. No. 1.7e-09; ive 0; Mismatches 1; Indels Query Match
Best Local Similarity 95.7.
Best Local 22, Conservative

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ò g RESULT 15

ABG74783 standard; protein; 347 AA. ABG74783;

(first entry) 05-JUN-2003 Human CH2-human/canine CH3-human CH4 IgE-3 fusion protein.

CH3 domain; IgE; antigen; non-anaphylactic; anti-IgE; fusion protein; dermatological; allergy; asthma; allergy; rhinitis; gastrointestinal allergy; food allergy; eosinophilia; conjunctivitis; glomerular neghritis; flea allergy; atopic dermatitis; gene therapy; human; canine; dog.

Canis familiaris. Ношо

EP1262491-A2

22-MAY-2002; 2002EP-00253606.

22-MAY-2001; 2001US-0292638P.

(PFIZ) PFIZER PROD INC

Morsey MA; Brown TM,

WPI; 2003-122561/12. N-PSDB; ACA55181 Novel isolated antigenic peptide comprising amino acid residues of CH3 domain of IgE molecule from first species and a second unrelated species, induces non-anaphylactic anti-IgE immune response in animal.

Claim 3; Page 37-39; 50pp; English.

This invention describes a novel antigenic peptide comprising amino acid residues of an IGE CH3 domain from a first species (ADE1) and amino acid residues of an IGE CH3 domain of a second unrelated species (ADE2), where ADE1 is conserved in the IGE CH3 domain of the second species and ADE2 is not conserved in the IGE CH3 domain of the first species. The novel antigenic peptide induces a non-anaphylactic anti-IGE immune response in

an antique, the invention also discusses the purposed councillation protein comprising the antigenic peptide and an antigenic protein comprising the antigenic peptide of the invention and a heterologue protein carrier, where the fusion protein induces an anti-1gE immune response that does not cause anaphylaxis when administered to an animal. The products of the invention have dermatological, antiinflammatcry and protein induces an animal. The products of the invention protein peptide described is capable of preventing 1gE from binding to high affinity receptors on mast calls and basophils. The products of the invention are useful in the manufacture of a medicament for treating or preventing 1gE-mediated allergies uncluding asthma, allergic rhinitis, gastrointestinal allergies uch as including asthma, allergic rhinitis, an animal, e.g. human or dog. The polynucleotide products are useful for treating 1gE-mediated allergic disorders of isorders, by gene therapy. Antigenic peptides comparising conserved amino acid residues of the CH3 domain of an 1gE molecule from a second unrelated species are capable of inducing a high causing anaphylaxis. ABG/4772-ABG/4785 represents polypeptide sequences used in designing the constructs described in the disclosure of the The invention also discloses the polynucleotide sequence invention

Sequence 347 AA;

Gaps ö Length 347; Score 118, DB 6, Length 34 Pred. No. 1.7e-09; 0; Mismatches 1; Indels Query Match
Best Local Similarity 95.7%;
Matches 22; Conservative

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à 유 completed: February 26, 2004, 08:23:34 Job time : 47.6 secs Search

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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-genic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (nonanaphylaxic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.
New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy; asthma; eczema; immunogenic peptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic polypeptides useful for preventing the harmful effects immunoglobulin \boldsymbol{E} in mammals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 118; DB 3; Length 31
Pred. No. 1.5e-09;
0; Mismatches 1; Indels
                                                    Example 1; Page 66-68; 155pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                187 GETYYCRVTHPHLPKDIVRSIAK 209
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Best Local Similarity 95.7%;
Matches 22; Conservative
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 312 AA;
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22-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chimeric
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The present sequence is an immunogenic peptide consisting of the heavy

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated antigenic peptide comprising amino acid residues of CH3 domain of IgE molecule from first species and a second unrelated species, induces non-anaphylactic anti-IgE immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH3 domain, IgE, antigen, non-anaphylactic; anti-IgE; fusion protein, dermatological; antiinflammatory; ophthalmological; allergy; asthma; allergic rhinitis; gastrointestinal allergy; food allergy; eosinophilia; conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis; gene therapy; human; canine; dog.
chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the dog. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthm, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)
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0
                                                                                                                                                                                                                               Length 341;
                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human IgE CH2-canine CH3-human CH4 IgE-1 fusion protein.
                                                                                                                                                                                                                               Score 118; DB 3;
Pred. No. 1.7e-09;
                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 206 GETYYCRVTHPHLPKDIVRSIAK 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABG74781 standard; protein; 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-MAY-2002; 2002EP-00253606.
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                                                                                                                                                                                                                            Query Match
Best Local Similarity 95.7%;
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Canis familiaris
                                                                                                                                                                                          Sequence 341 AA;
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EP1262491-A2

Synthetic.

Canis

04-DEC-2002

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Canine immunoglobulin B peptide fragment and related DNA - useful for the preparation of anti-canine immunoglobulin E antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is a partial canine immunoglobulin E (IGE) protein. Peptide fragments (AAW24098-106) containing at least five continuous amino acids of this sequence are used for the preparation of anti-canine IGE antibody. The anti-canine IGE antibody can be used for the diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Immunoglobulin B; 1gE; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitôpe; antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.
                                                                    Immunoglobulin E, IgE; anti-canine IgE antibody; allergy; canine; dog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.7%; Score 118; DB 2; Length 124;
llarity 95.7%; Pred. No. 5.2e-10;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dog immunoglobulin E epsilon heavy chain SEQ ID NO:2.
                     Partial canine immunoglobin E protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 8; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US013959.
                                                                                                                                                                                                                                                                       95JP-00334381
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N-PSDB; AAT85646.
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les 22; Conserv
                                                                                                                   Canis familiaris.
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                                                                                                                                                                                                                                                                    ^22-DEC-1995;
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                                                                                                                                                                                                                     30-JUN-1997.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a novel antigenic peptide comprising amino acid residues of an IGE CH3 domain from a first species (ADE1) and amino acid residues of an IGE CH3 domain of a second unrelated species ADE2; where CC ADE1 is conserved in the IGE CH3 domain of the second species and ADE2 is not conserved in the IGE CH3 domain of the first species. The novel antigenic peptide induces a non-anaphylactic anti-IGE immune response in an animal. The invention also discloses the polymucleotide sequence encoding the antigenic peptide and an antigenic fusion protein comprising the antigenic peptide and an antigenic fusion protein comprising carrier, where the fusion protein induces an anti-IGE immune response to the antigenic peptide of the invention and a heterologous protein carrier, where the fusion protein induces an anti-IGE immune response to the invention have dermatological, antiinflammatory and ophthalmological activity. The antigenic peptide described is capable of preventing IGE from binding to high affinity receptors on mast cells and ophthalmological activity. The invention are useful in the manufacture of a medicament for traating or preventing IGE-mediated allergies such as including asthma, allergic rhinitis, gastrointestinal allergies such as including asthma, allergic rhinitis, gastrointestinal allergies such as allergic dermatitis, in an animal, e.g. human or dog. The polyuncleotide products are useful for treating IGE-mediated allergic disorders, by gene therapy. Antigenic peptides comprising conserved amino a second unrelated species are capable of inducing a high content of anti-IGE antibodies when administered to an animal without causing anaphylaxis. ABG74772-ABG7478 sepresents polypeptide sequences conserved in unclaing anaphylaxis. ABG74772-ABG7478 in the disclosure of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated antigenic peptide comprising amino acid residues of CH3 domain of IgE molecule from first species and a second unrelated species, induces non-anaphylactic anti-IgE immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 GETYYCRVTHPHLPKDIVRSIAK 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Page 29; 50pp; English.
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                                                                                                                                                                                                                     22-MAY-2002; 2002EP-00253606.
                                                                                                                                                                                                                                                                       22-MAY-2001; 2001US-0292638P
                                                                                                                                                                                                                                                                                                                    (PFIZ ) PFIZER PROD INC
                                                                                                                                                                                                                                                                                                                                                                      Brown TM, Morsey MA;
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-122561/12.
N-PSDB; ACA55171.
                                               familiaris.
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WPI; 2000-160578/14.

(first entry)

21-NOV-1997

AAW24097;

RESULT 11 AAW24097

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Gaps

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This invention describes a novel antigenic peptide comprising amino acid residues of an IgE CH3 domain from a first species (ADE1) and amino acid residues of an IgE CH3 domain of a second unrelated species (ADE2), where ADE1 is conserved in the IgE CH3 domain of the second species and ADE2 is antigenic peptide induces a non-anaphylactic anti-ige immune response in animal. The invention also discloses the polymuclecitide sequence an animal. The invention also discloses the polymuclecitide sequence concoding the antigenic peptide and an antigenic peptide of the invention and a heterologous protein comprising the antigenic peptide of the invention and a heterologous protein carrier, where the flusion protein induces an anti-ing immune response that does not cause anaphylaxis when administered to an animal. The products of the invention have dermatological, antiinflammatory and ophthalmological activity. The antigenic peptide described is capable of preventing IgE from binding to high affinity receptors on mast cells and ophthalmological activity. The antigenic peptide described is capable of preventing IgE from binding to high affinity receptors on mast cells and ophthalmological activity. The antigenic peptide allergies confers including athema, allergic rhintis, gastrointestinal allergies confers including athema, allergic rhintis, gastrointestinal allergic seconds allergic conserved amino additional described in an animal, e.g. human or dog. The polymucleotide products are useful for treating IgE-mediated allergic additional and described and animo additional and described and animo additional and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and described and d
                                                                                                       Novel isolated antigenic peptide comprising amino acid residues of CH3 domain of IgE molecule from first species and a second unrelated species, induces non-anaphylactic anti-IgE immune response in animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          molecule from a second unrelated species are capable of inducing a high titre of anti-1gs antibodies when administered to an antihal without causing anaphylaxis. ABG7472-ABG74785 represents polypeptide sequences used in designing the constructs described in the disclosure of the
                                                                                                                                                                                                                                                     Claim 15; Page 28; 50pp; English.
WPI; 2003-122561/12.
N-PSDB; ACA55170.
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Sequence 114 AA;

Query Match 83.7%; Score 118; DB 6; Length 114; Best Local Similarity 95.7%; Pred. No. 4.7e-10; Matches 22; Conservative 0; Mismatches 1; Indels 2 GETYYSRVTHPHLPKDIVRSIAK 24

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0; Gaps

84 GETYYCRVTHPHLPKDIVRSIAK 106

ABG74774 standard; protein; 115 AA ABG74774; RESULT 9 ABG74774

(revised)
(first entry) 23-OCT-2003 05-JUN-2003

Human IgE CH3 domain-canine CH3 domain chimeric construct.

CH3 domain; IgB; antigen; non-anaphylactic; anti-IgB; fusion protein; dermatological; altinfilammatory; ophthalmological; allergy; asthma; allergy; asthma; allergy; asthma; conjunctivitis; gastrointestinal allergy; food allergy; eosinophilis; conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis; gene therapy

Homo sapiens. Canis familiaris.

Chimeric.

EP1262491-A2

04-DEC-2002

22-MAY-2002; 2002EP-00253606.

22-MAY-2001; 2001US-0292638P.

(PFIZ) PFIZER PROD

Brown TM, Morsey MA;

WPI; 2003-122561/12. N-PSDB; ACA55172.

Novel isolated antigenic peptide comprising amino acid residues of CH3 domain of IgE molecule from first species and a second unrelated species, induces non-anaphylactic anti-IgE immune response in animal.

Claim 2; Page 29-30; 50pp; English.

This invention describes a novel antigenic peptide comprising amino acid residues of an IgB CH3 domain from a first species (ADE1) and amino acid residues of an IgB CH3 domain from a first species (ADE2), where ADE1 is conserved in the IgE CH3 domain of the second species and ADE2 is not conserved in the IgE CH3 domain of the first species. The novel antigenic peptide induces a non-anaphylactic anti-IgE immune response in a manimal. The invention also discloses the polynucleotide sequence encoding the antigenic peptide and an antigenic fusion protein comprising the antigenic peptide of the invention and a heterologous protein concing the antigenic peptide and antigenic peptide of the invention and a heterologua protein carrier, where the fusion protein induces an anti-IgE immune response that does not cause anaphylaxis when administered to an animal. The products of the invention and a heterologua protein cophthalmological activity. The antigenic peptide described is capable of preventing IgE from binding to high affinity receptors on mast cells and opphthalmological activity. The antigenic peptide described is capable of preventing IgE from binding to high affinity receptors on mast cells and basophils. The products of the invention are useful in the manufacture of a medicament for treating or preventing IgE-mediated allergic disorders including asthma, allergic rhinitis, gastrointestinal allergies such as food allergies of the CH3 domain of an IgE molecule from a second unrelated species are capable of inducing a high colling assidues of the CH3 domain of an IgE molecule from a second unrelated species are capable of inducing a high current of antibodies when administered to an animal without causing anaphylaxis. ABG7472-ABG7478 Epresents polypeptide sequences conserved in designing the constructs described in the disclosure of the current of Updated on 23-OCT-2003 to standardise of field of the constructs described in the disclosure of the

Sequence 115 AA;

Gaps ; 0 Length 115; / Match 83.7%; Score 118; DB 6; Length 11 Local Similarity 95.7%; Pred. No. 4.8e-10; nes 22; Conservative 0; Mismatches 1; Indels Query Match Best Loca Matches

24 GETYYSRVTHPHLPKDIVRSIAK N

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GETYYCRVTHPHLPKDIVRSIAK 107 82 RESULT 10 ABG74773

ABG74773 standard; protein; 117 AA

05-JUN-2003 (first entry)

ABG74773;

Human IgB CH3 domain-canine CH3 domain fusion construct.

CH3 domain; IgE; antigen; non-anaphylactic; anti-IgE; fusion protein; dermatological; antiinflammatory; ophthalmological; allergy; asthma; allergy chinitis; gastrointestinal allergy; food allergy; eosinophilia; conjunctivitis; glomerular nephritis; flea allergy; atopic dermatitis; gene therapy; human; dog.

29-DEC-1999

Wang CY,

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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenties reflector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maphylactogenic) antibodies. Apty9994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                   New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
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100.0%; Pred. No. 7.2e-14;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 14; Page 77; 155pp; English
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                                                                                                       (UNBI-) UNITED BIOMEDICAL INC.
                                  98US-00100287.
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                                                                                                                                                                             walfield AM;
                                                                                                                                                                                                                                                  WPI; 2000-160578/14.
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Best Local Similarity
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                                  20-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
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                                                                                                                                                                                                                                                                                                                                                                                                (UNBI-) UNITED BIOMEDICAL INC.
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Best Local Similarity 100.
Matches 25; Conservative
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                                  Unidentified
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Morsey MA;

Brown TM,

99WO-US013959

21-JUN-1999;

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W09967293-A1

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AAY80084;

AAY80084 RESULT

Length 63; Indels

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The present invention describes immunoglobulin E (1gE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-anaphylactic and anti-anaphylactic anti-argentist properties. (I) induces polyclonal antibodies specific for a target effector site on the epsilon-heavy chain of IgE, and so containing triggering and activation of mast cells and basophils and command (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, aethma, anaphylaxis, or flea-allergy containing (I) are used for active immunisation against IgE-mediated allergies, e.g. food allergies, aethma, anaphylaxis, or flea-allergy commission broadction of corresponding peptides or in DRA vaccines. Tecombinant production of corresponding peptides or in DRA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope (functional in agentically diverse subjects), in addition to a B cell carget epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY19094 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
                                                                                                             Immunoglobulin E, IgE, epsilon heavy chain, antigenic; antigen; immunogranic; immunostimulatory; carrier protein; helper T cell epitope, antibody; allergy; allergic disease; immunisation; anti-allergic; anti-anaphylactic; athma; asthma; anaphylactic; attmatic; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.
                                                        IgE immunogenic peptide conjugate SEQ ID NO:88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UNBI-) UNITED BIOMEDICAL INC
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15-MAY-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                IgE immunogenic peptide conjugate SEQ ID NO:27.
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                                                                                                                          AAY80020 standard; peptide; 46 AA.
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Matches 25; Conservative
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                                  Gaps
                                                                                                                                                                                                                                                                                                   Immunoglobulin E; IgE; epsilon heavy chain; antigenic; antigen;
                                  .
0
 Length 57;
                               Indels
 100.0%; Score 141; DB 3;
100.0%; Pred. No. 6.4e-14;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                     IgE immunogenic peptide conjugate SEQ ID NO:87.
                                                                1 CGETYYSRVTHPHLPKDIVRSIAKC 25
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                                                                                      CGETYYSRVTHPHLPKDIVRSIAKC
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                                                                                                                                                                           AAY80080 standard, peptide; 62
                                                                                                                                                                                                                                         (first entry)
                                  25; Conservative
Query Match
Best Local Similarity
Matches 25; Conserv
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AAY80081 standard; peptide; 57

RESULT 5

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AAY80081

AAY80081

Length 45;

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The present invention describes immunoglobulin E (IGE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and a target effector site on the epstlon-heavy chain of IGE, and so preventing triggering and activation of mast cells and basophils and downergulation of IGE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IGE-mediated allergies, e.g. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscious T helper cell epitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (nonanaphylaxica) antibodies. AAY19994 to AAX80084 represent amino acid sequences used in the exemplification of the present invention
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(functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (non-anaphylactogenic) antibodies. AAY79994 to AAY80084 represent amino acid sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                              100.0%; Score 141; DB 3; Length 25; 100.0%; Pred. No. 2.4e-14; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                       AAY80019 standard; peptide; 45
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                                                                                                                                                                                                   Best Local Similarity
Matches 25; Conserv
                                                                                                                                            Sequence 25 AA;
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Sequence 45 AA;

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The present invention describes immunoglobulin E (IgE)-CH3 domain antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and antigenic properties. (I) induces polyclonal antibodies specific a target effector site on the epsilon-heavy chain of IgE, and so preventing triggering and activation of mast cells and basophils and downregulation of IgE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against IgE-mediated alergies, eg. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. (Conjugates of (I) that include a promiscuous T helper cell apitope (functional in genetically diverse subjects), in addition to a B cell target epitope, have increased immunogenicity and may include cyclic constraints (disulfide bridge) to stabilise conformational features and maximize cross-reactivity to the natural target. They induce safe (nonaphylactogenic) antibodies, AAV79994 to AAX80084 represent amino acid
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                                   Indels
; DB 3;
4.9e-14;
                                                                                                                                                                                                                                                                                              IgE immunogenic peptide conjugate SEQ ID NO:90.
                                 Mismatches
100.0%; Score 141;
100.0%; Pred. No. 4
ive 0; Mismatche
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                                                                    1 CGETYYSRVTHPHLPKDIVRSIAKC
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                                                                                                                                                                                             AAY80083 standard; peptide;
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Query Match
Best Local Similarity 100.
Matches 25; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified.
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                                                                                                                                                            RESULT 3
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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February 26, 2004, 08:16:50 ; Search time 46.6 Seconds (without alignments) 151.581 Million cell updates/sec Run on:

1 CGETYYSRVTHPHLPKDIVRSIAKC 25 US-09-701-623C-6 141 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 Total number of hits satisfying chosen parameters:

1586107 segs, 282547505 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* A_Geneseq_29Jan04: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	10n	_	IgE immun		IgE immun	Н	н	IgE immun	U	Human	Human	Partia	Dog immun	,	Human 1gE	Human CH2	Human CH2	Canine Ig	Canine I		Pept					Modified
	Description	Aay79999	Aay80019	Aay80083	Aay80020	Aay80081	Aay80080	Aay80084	Abg74772	Abg74774	Abg74773	Aaw24097	Aay79995	Aab06208	Abg74781	Abg74783	Abg74782	Aaw23067	Aar97753	Abp96583	Aay68602	Aay91212	Aay79998	Aay68604	Aay91216	Aay91215
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	a :	AAY7999	AAY80019	AAY8008	AAY8002	AAY8008	AAY8008	AAY80084	ABG7477	ABG74774	ABG7477	AAW24097	AAY79995	AAB06208	ABG74781	ABG7478	ABG74782	AAW23067	AAR97753	AB P9658	AAY68602	AAY9121	AAY7999	AAY68604	AAY9121	AAY9121
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,	rengtn	25	4.0	4.5	46	57	62	63	114	115	117	124	312	341	346	347	348	417	426	426	25	25	25	42	42	42
Query	March	100.0	100.0	100.0	100.0	100.0	100.0	100.0	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	83.7	76.6	76.6	76.6	76.6	76.6	9.94
Ċ	Score	141	141	141	141	141	141	141	118		118	118		118	118	118	118	118	118	118	108	108	108	108	108	108
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	Aay8001		Pept				Aay68603 Peptide s		Aay91214 Modified	Aay80011 IgE immun	9	0	Aay80013 IgE immun	Aay80015 IgE immun	Aay68606 Peptide s	Aay91219 Inv epito	Ige	Aay80012 IgE immun	Aay80077 Optimised	
AAY91217	AAY80014	ADD89950	AAY68605	AAY91218	AAY80007	ADD89951	AAY68603	AAY91213	AAY91214	AAY80011	AAY80016	AAY80010	AAY80013	AAY80015	AAY68606	AAY91219	AAYBOOOB	AAY80012	AAY80077	
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76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	74.5	
108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	108	105	
26		28				32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

Optimised IgE-CH3 domain antigen peptide for dog IgE. AAY79999 standard; peptide; 25 AA. 15-MAY-2000 (first entry) AAY79999; RESULT 1

Immunoglobulin B; IgB; epsilon heavy chain; antigenic; antigen; immunogenic; immunostimulatory; carrier protein; helper T cell epitope; antibody; allergic disease; immunisation; anti-alergic; anti-anaphylactic; anti-asthmatic; asthma; anaphylaxis; dermatitis.

Canis sp. Synthetic.

W09967293-A1

29-DEC-1999.

99WO-US013959. 21-JUN-1999; 98US-00100287. 20-JUN-1998; (UNBI-) UNITED BIOMEDICAL INC.

Wang CY, Walfield AM;

WPI; 2000-160578/14.

New antigenic peptide from the CH3 domain of immunoglobulin E, fusions for immunization against allergy.

Claim 1; Page 99; 155pp; English.

for antigenic peptides (I). (I) have anti-allergic, anti-anaphylactic and anti-asthmatic properties. (I) induces polyclonal anti-bodies specific at target effector site on the epsilon-heavy chain of 1gE, and so preventing triggering and activation of mast cells and bacophils and downregulation of 1gE synthesis. Conjugates, or fusion peptides, containing (I) are used for active immunisation against 1gE-mediated allergies, eg. food allergies, asthma, anaphylaxis, or flea-allergy dermatitis. Nucleic acids that encode these compounds are useful for recombinant production of corresponding peptides or in DNA vaccines. Conjugates of (I) that include a promiscuous T helper cell epitope present invention describes immunoglobulin E (IgE)-CH3 domain

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21 CGETYQSRVTHPHLPRALMRSTTKC 45
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US-10-355-161A-11
Sequence 11, Application US/10355161A
Sequence 11, Application US/10355161A
Publication No. US20040009897A1
GENERAL INFORMATION:
APPLICANT: Sokol), Kenneth K.
ITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
FILE REPERENCE: Immunogen Delivery System
CURRENT APPLICATION NUMBER: US/10/355,161A
CURRENT APPLICATION NUMBER: US/10/355,161A
PRIOR FILING DATE: 2003-01-31
PRIOR FILING DATE: 2003-01-44
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
LENGTH: 45
                                                                                                                                                                                                                                              RESULT 12
US-10-076-674-11
Sequence 11, Application US/10076674
Publication No. US20030165478A1
GENERAL INFORMATION:
TITLE OF INVENTION: Kenneth K.
TITLE OF INVENTION WUMBER: US/10/076,674
CURRENT FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 11
SOFTWARE: Patentin version 3.1
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                                                                DB 15; Length 44;
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71.0%; Score 103; DB 14; Length 45;
Best Local Similarity 68.0%; Pred. No. 2.1e-07;
Matches 17; Conservative 3; Mismatches 5; Indels
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                                                            Query Match
71.0%; Score 103; DB 15
Best Local Similarity 68.0%; Pred. No. 2e-07;
Matches 17; Conservative 3; Mismatches
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| LOCATION: (20)...(20)
| OTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-355-1618-11
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US-10-355-161A-10
                                                                                                                                                                       20 CGETYQSRVTHPHLPRALMRSTTKC 44
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                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
CNGANTSM: mus musculus
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (1)...(332)
CTHER INFORMATION: Murine IGE heavy chain domains C2, C3, and US-09-949-375A-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.6%; Score 98; DB 9; Length 332; Best Local Similarity 82.6%; Pred. No. 8.5e-06; Matches 19; Conservative 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 25, Application US/09949375A; Patent No. US20020172673A1; Patent No. US20020172673A1; Patent No. US20020172673A1; GENERAL INFORMATION: APPLICANT: KLYSNER, Steen et al.; TITLE OF INVENTION: METHOD FOR DOWN-REGULATING IGE: FILE REFERENCE: 3631-0111P; CURRENT APPLICATION UNMER: US/09/949,375A; CURRENT FILLING DATE: 2002-01-18; NUMBER OF SEQ ID NOS: 38; SOUTHARE: PatentIn version 3.1; SEQ ID NO 25; LENGTH: 332; TYPE: PRT

CURRENT APLICATION VERSION 3.1; SEQ ID NO 25; LENGTH: 332

TYPE: PRT

PRATURE: PRT

PRATURE: PRT
US-09-949-375A-23
US-09-949-375A-23
Sequence 23, Application US/09949375A
February CUS20020172673A1
GENERAL INFORMATION: Steen et al.
APPLICAMY: KUTSNER, Steen et al.
TITLE OF INVENTION: WITHOD FOR DOWN-REGULATING IGE
FILE REFERENCE: 3631-0111P
CURRENT APPLICATION WINGHER: US/09/949,375A
CURRENT APPLICATION WINGHER: US/09/949,375A
CURRENT APPLICATION WINGHER: 1202-01-18
NUMBER OF SEQ ID NOS: 38
SOFURARE: PATENTIN VERSION 3.1
SEQ ID NO 23
LENGTH: 332
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CURRENT APPLICATION NUMBER: US/10/214,524
CURRENT FILING DATE: 2002-08-08
PRIOR APPLICATION NUMBER: 60/312,120
PRIOR FILING DATE: 2001-08-13
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.1
LENGTH: 428
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                                                                                                                                                     TYPE: PRT;
; ORGANISM: Rat (Rattus norvegicus)
US-10-214-524-34
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LOCATION: (19)..(19)
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ORGANISM: Human
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US-10-076-674-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 14, Application US/10152190
Publication No. US20030096369A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: No. US20030096369A1-anaphylactogenic IgE vaccines
FILE REPERENCE: PC11011A
CURRENT APPLICATION NUMBER: US/10/152,190
CURRENT FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 84.1%; Score 122; DB 14; Length 346; Local Similarity 95.7%; Pred. No. 3.6e-09; nes 22; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

84.1%; Score 122; DB 14; Length 341;

Best Local Similarity 95.7%; Pred. No. 3.6e-09;

Matches 22; Conservative 0; Mismatches 1; Indels
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US-10-176-664-9
                                                                   212 GEGYQCRVDHPHFPKPIVRSITK 234
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Publication No. US20030073142A1
GENERAL INFORMATION:
APPLICANT: Chen, Swey-Shen Alex
APPLICANT: Yang, Yong-Min
APPLICANT: Barankiewicz, Theresa J.
APPLICANT: Chen, Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT; ORGANISM: IGE-5 fusion protein US-10-152-190-14
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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Best Local S:
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Publication No. US20040009897A1

GENERAL INFORMATION:

APPLICANT: SOKO1, Kenneth K.

TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System

TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System

FILE REFRENCE: Immunogen Delivery System

CURRENT APPLICATION NUMBER: US/10/355,161A

CURRENT APPLICATION NUMBER: US 10/076674

PRIOR FILING DATE: 2002-02-14

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin version 3.1

SEQ ID NO 10
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Sequence 10. Application US/10076674

GENERAL INFORMATION:

APPLICANT: Sokol1, Kenneth K.

APPLICANT: Sokol1, Kenneth K.

TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System

FILE REPERENCE: Immunogen Delivery System

CURRENT FILING DATE: 2002-04-23

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.1

SEQ ID NO 10

LENGTH: 44
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   Length 428;
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Query Match
84.1%; Score 122; DB 14;
Best Local Similarity 95.7%; Pred. No. 4.5e-09;
Matches 22; Conservative 0; Mismatches 1;
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NAME/KEY: misc feature
LOCATION: (19)...(19)
COTHER INFORMATION: Xaa indicates epsilon-Lys
US-10-076-674-10
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Length 341;
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                                              Query Match 84.1%; Score 122; DB 9; Length 341; Best Local Similarity 95.7%; Pred. No. 3.6e-09; Matches 22; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Synthetically generated proteins
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84.1%; Score 122; DB 14;
Best Local Similarity 95.7%; Pred. No. 3.6e-09;
Matches 22; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hellman, Lars T.
APPLICANT: Hellman, Lars T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/09/401,636
CURRENT FILING DATE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1998-11-02
PRIOR FILING DATE: 1998-11-02
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
ENDING 1341
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Sequence 4, Application US/10176664

Publication No. US2003003163A1

SEDERAL INFORMATION:
APPLICANT: Hellman, Lars T.
TITLE OF INFORTION: ENHANCED VACCINES
FILE REFERENCE: 1022/006001

CURRENT FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: US/09/401,636

PRIOR APPLICATION NUMBER: US/09/401,636

PRIOR APPLICATION NUMBER: US/09/401,636

PRIOR PELING DATE: 1999-09-22

PRIOR PELING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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LENGTH: 341
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          US-09-401-636-4
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84.1%; Score 122; DB 14; Length 340;
Best Local Similarity 95.7%; Pred. No. 3.6e-09;
Matches 22; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                          Length 340;
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84.1%; Score 122; DB 9; Length 34

Best Local Similarity 95.7%; Pred. No. 3.6e-09;

Matches 22; Conservative 0; Mismatches 1; Indels
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FEATURE:
OTHER INFORMATION: Synthetically generated proteins
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; OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-2
                                                                                                                                                                                               , OTHER INFORMATION: Synthetically generated proteins US-09-401-636-2
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Patent No. US20010038843A1
GENERAL INFORMATION:
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT FILING DAIE: 1999-09-22
PRIOR APPLICATION NUMBER: US 60/106,652
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1999-11-02
PRIOR FILING DATE: 1998-11-02
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10176664
; Publication No. US20030031663A1
; GENERAL INFORMATION:
APPLICANT: Hellman, Larg T.
TITLE OF INVENTION: ENHANCED VACCINES
FILE REFERENCE: 10223/006001
CURRENT APPLICATION NUMBER: US/10/176,664
; CURRENT FILING DATE: 1999-09-22
PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
LENGTH: 340
PRIOR FILING DATE: 1998-11-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 340
TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-176-664-2
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LENGTH: 341
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US-09-401-636-4
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Sequence 5, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 9, Appli	Sequence 4, Appli	Seguence 9, Appli	Sequence 14, Appl	Sequence 34, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 11, Appl	Sequence 11, Appl	Sequence 23, Appl	Sequence 25, Appl
SUMMARIES	ΙD	US-10-152-190-5	US-09-401-636-2	US-10-176-664-2	US-09-401-636-4	US-09-401-636-9	US-10-176-664-4	US-10-176-664-9	US-10-152-190-14	US-10-214-524-34	US-10-076-674-10	US-10-355-161A-10	US-10-076-674-11	US-10-355-161A-11	US-09-949-375A-23	US-09-949-375A-25
	DB	14.	σ	14	σι	σ	14	14	14	14	14	15	14	12	σ	σ
	% Query Match Length DB	114	340	340	341	341	341	341	346	428	44	44	45	45	332	332
	% Query Match	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	84.1	71.0	71.0	71.0	71.0	67.6	67.6
	Score	122	122	122	122	122	122	122	122	122	103	103	103	103	96	86
	Result No.		7	m	4.	Ŋ	9	7	80	σ	10	11	12	13	14	15

US-00-401-636-2 Sequence 2, Application US/09401636 Fatent No. US20010038843Al GENERAL INFORMATION: APPLICANT: Hellman. Lars T. ITLE OF INVENTION: ENHANCED VACCINES FILE REFERENCE: 10223/006001 CURRENT APPLICATION NUMBER: US/09/401,636 CURRENT PLING DATE: 1999-09-22 PRIOR APPLICATION NUMBER: US 60/106,652

84 GEGYÇCRVDHPHFPKPIVRSITK 106

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2 GEGYQSRVDHPHFPKPIVRSITK

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Sequence 6, Appli Sequence 6, Appli Sequence 20, Appli Sequence 22, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 13, Appl Sequence 14, Appli Sequence 26, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 21, Appli Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 24, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli	ogenic IgB vaccines
US-09-949-375A-27 US-09-401-664-6 US-09-949-375A-20 US-09-949-375A-22 US-09-949-375A-22 US-09-949-375A-22 US-09-949-375A-12 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	ALICOMMENTS 152190 A1 330096369A1-anaphylactogeni US/10/152,190 5-21 5-21 ; Score 122, DB 14; Leng
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